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Xu,H., Swoboda,I., Bhalla,P.L. and Singh,M.B.
Direct Submission
Submitted (03-DEC-1998) Environmental Horticulture and Resource
Male qumetic rell'specific gene expression in Howering plants
Proc. Natl Arad. Sci. U.S.A. 96 (5), 2554-2558 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-NOV 1998) The Institute [11 General h. Medical Genter Drive, Esekellie, M. 10814, USA
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/wene="PPRG27nw"
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/protein_id="AAC71845.1"
/db_xref-"GI:3845142"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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0; Mismarches 67.
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                                                                                                                                                             Berlin-Charlottenburg, GERMANY; Email: elone=rzpd.de Further
information about the clone and the sequencing project is available
at http://www.nijs.lib.ben.mpf.bc.proj/2002/1
[Accation/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Laus Lallon = "LNVEKCDINEPTAYHFIRRYAM" (HINMATELLSKY JCEMTLOG
YHYVOEKASKI AAASILI ALYMKKI GYWVPFI BHYSGYSTSEL HPLVP-CLNELLI PSS
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The Sanger Centre, Wellcome Trust Genome Campus, Hinzton, Cambridge
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Close than & Wisherman Melocular Coronno Amalysis degraes Puncar Research Center (5875). Email 8.winmans GALZ benidelbers de sequenced by Medifore mix (Martinstied/Sermany) within the eDNA sequenced by Medifore mix (Martinstied/Sermany) within the eDNA sequenced by Medifore mix (Martinstied/Sermany) within the eDNA sequenced by Medifore mix (MRZDA 440825) is available at the EZDD in Berlin, Please contact the EZDD Ressourcescentrum, Heubnerwey 6, 18059
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Bownan, S., Chrecher, C., Harris, B., Barris, D., Lawsen, U., Ouali, M. and Barrell, B.
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sequence is unfiltabled and dows not necessarily represent the
correct sequence. Work on the sequence is in progress and the
release of this data is based on the understanding that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T7 end of clone AX0AA017D07 of library AX0AA from strain CBS 7054 AL4404Ha farinosa, sequence tagged site.
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For more information about this sequence or the Malaria Project
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Wincker, P., Artiquenave, F. and Potier, S.
Genomic Exploration of the Hemiascomycetous Yeasts: 15. Pichia
                                                                                                                                                   Segmence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Caps
                                                                                                                                                                                                                                                     • Note this is a weeken furth sequence.
• This record will be applated with the traishot sequence.
• as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                           Order of segments is not known; 800 n's separate segments.
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Souciet, J.L., Aigle, M., Artiquenave, F., Blandin, G.
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Submitted (07-SEP-ZUUA) Generape - Centre National de Sequencare,
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Pterygota, Newtera, Endopterygota; Dipt.co. Reformation
Muscomorpha, Ephydroidea; Drosophilidae; Drosophila.
1 (pascs 1 to 2719)
Bickel,S.E., Wyman,D.W., Miyazaki,W.Y., Moore,D.P. and
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Orr-Weaver, T.L.
Identification of ven, a brosophila protein essential for sister
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/db_vrcf "(acon.7227"
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/product."ORD protein"
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                                                                                                                       LMBs J. 15 (6), 1451-1459 (1996)
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Superiorien Cremions, CP 2706, 40272 SVPF o. E.

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Boloti Fukuhara, M., Bon, E., Brottier, P., Casareqola, S.,
de-Montique, J., Dujon, H., Durrens, P., Lopindie, A., Horente, B.,
Malpertuy, A., Neuweglise, C., Ozier-Kalogeropoulos, G., Potier, S.,
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goust species for molecular evolution studies(1)
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Wincker, P. and Weissenbach, J.
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Direct Submission
Submitted (06-MAY-1954) Joseph L. Dynes, Department of Biology,
University of California, Center for Molecular Genetics, San Blogo,
CA 42093-0834, USA
1.2974, 1.3476
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                                                                                         773 AWAWTAAATAATTHTTAAWTWAAWMTTTTWWWWWWWAHTANAAATATTTTTT 832
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Firtel,R.A.
508 ittitaetgaacialtidaltititeaatitieaesaaaaatiatidalaalgaaatgi 567
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1 (bases 1 to 2976)
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/strain "KAx-?"
/db_xret="taxon:44689"
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/1956 "Tage"
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/qene -"TagG"
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/1600 "TaqC"
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Submitted (15-MAR-1999) P.falciparum Genome Sequencing Consentium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambildge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bowman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quall, M. and Barrell, B.
                                                                                                                                                                                        tocaletticagraticaticagetetgatataaaattyeteritaayyayaaaalletaylig 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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* This record will be updated with the finished sequence.
                                                                                                      Smore 61.4; DB 6; Length 2976; Pred. No. 0.26;
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Plasmodium falciparum
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/chromosome="13"
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/product="unknown"
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Rivero,F., Dislich,H. and Noegel,A.A.
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Rivero,F., Dislich,H., Gloeckner,G. and Norgel,A.A.
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/protein_idd="AAGGS122.1"
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Kurdi,o.R., Comway.A.B. and Davis.R.W.
Plasmodium falciparum NP7 chromosome 12
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Hyman, R.W., Olin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
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Center, Stanford University, 855 California Avenue, Palo Alto, CA
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(T. A.4.) 13, 2000 this sequence version replaced gig8810450.
* NoTE: This is a 'working draft' sequence. If currently consists of leonings, Gaps between the confidence of a sum of N. The order of the pieces.
* is believed to be carrect as gives, however the sizes.
* of the gaps between them are based on estimates that have.

provided by the submittor.
This sequence will be replaced
by the thinkbed sequence us seen as it is available and
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the accession number will be preserved.

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/gene "mcm2"
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/Algared "taxon.5833"
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The Sanger Centre, Wellcome Trust Genome Campus, Histor, Cambridge
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Eukaryota, Alveolata, Apicomplexa, Haemusporida, Plasmodium.
1 (buses 1 to 224449)
Bowman S., Churcher, C., Harris, P., Harris, D., Lawson, D., Yuail, M. and Barrell, B.
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http://www.sanjor.ar.ub/Project/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.in/Project.i
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Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be
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Pred. No. 0.38;
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For more information about this sequence or the Maiaria Project, sectificity, www.sanget.ac.uk,Projects/l_dicipatas. AmcMrANI. This sequence is not the entire insert of clone MAL4P2. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Churcher, C., Harris, R., Harris, D., Lawson, D.
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Submitted (24-PEE-1999) P. falciparum Genome Sequencing Consortium,
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             * NOTE: This is a working draft' sequence.

* This revord will be updated with the finish d sequence.

* as soon as it is available and the avcession number will
Order of segments is not known; 800 n's separate segments.
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Zhote-"MALAP2.02, very hypothetical protein, Ten: 139 aa".
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John (6744 — 6864, 6851 — 887, 8454 — 8868, 8878 — 6699, 9746 — 10

10170 — 10259, 10349 — 10378, 10851 — 10766, 10776 — 10787)
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/protein_id="CAB62843.1"
/db_rost="c1.6562794"
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/de.drein_id="PANG$842_1"
/db_xrei="G16562703"
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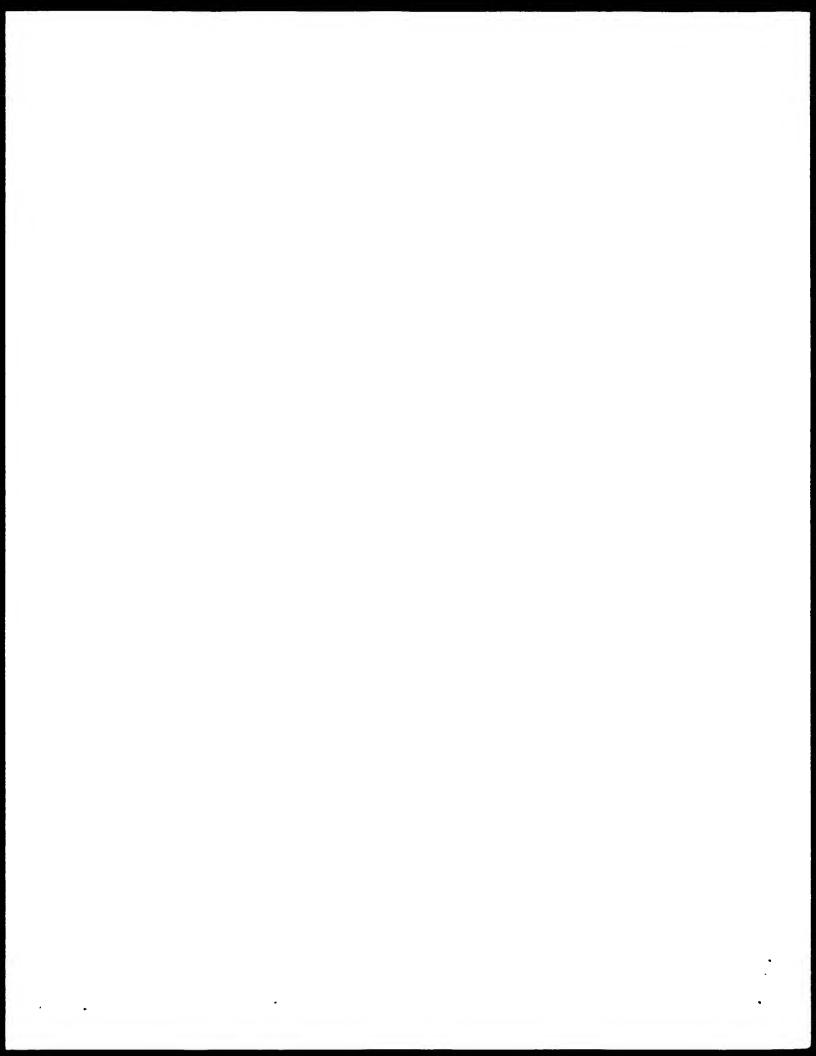
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350.1 KTURLALLI GNIKEFI LETIGALETI GRI FRI ATOTTI VERTRETO INITATOTI VERTRETO
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//note-"predicted splice donor sequence, acc/qtaaat, for excn 8 of MALAP2.03"
9645. 9650
//note-"alternative splice donor sequence, acc/qtaaat, for cxon 8 of MALAP2.03"
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MAL4P2.03"
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Justie "predicted splice acceptor sequence for exon 8 of
MAIAP2.03"
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11727. .11794,11978. .12324))
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Narbonne, 31062 Toulouse CEDEX, FRANCE
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South Teaching detection of management of the parameter of MAIAP2.03"
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74.5%; Pred. No. 0.37;
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Submitted (11-JUN-1997) D. Goffner, Centre de Biologie et
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11727, 11794,11978, 12324))
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                                                           ÄVSTCSS"GDFTI PVGSORTYMI ELLINAAI NEFI FFF LACHRI TVVFVIATYVRPFRT
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                                                                                                                                                                                                                                                                            9.6%, Score 60.2, DB 14; Length 1589;
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/protein_id "CAA/4101.1"
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352 C 294
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Search completed: July 22, 2601, 01:24:34 Job time: 1960 sec

1541 AAAAAAAAAAAAA 1557



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Etd.
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OM nucleic - nucleic search, using sw model

July 22, 2601, 06 23 09 , wasth time 52,77 Squards. (without alignments) 1248.654 Million cell quatus/seq Run on:

US-09-463-480-3 625 Title: Perfect score:

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TENTITY NIC Scoring table:

Gapop 10 0 . Gapext 1 0

Total number of hits satisfying chosen parameters.

317530 segs, 92630169 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_NA:*
//cquz_c7prodata//ina/5A_COMB.seq:*
//cquz_c7prodata///ina/6A_COMB.seq:*
//cquz_c7prodata///ina/6A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

		œ			SOMMANIES	
Result. No.	Score	Query Match	Length	DB	ID	Description
	58.6	4.2	857	-	115-08-308-883-1	Secure 1 Appli
7	20.00	4	0 00	-	-08-7-08-7-63	
l an	28.6	2	80.07	4 7	08-256-799	Sequence 1, Appril
4	58.6	9.6	857	4	-08-462-	-
ر 5	58.2	6	3138	_	-07-867-10	Sequence 1, Appli
9	56.8	6.1	991	æ	US-08-924-747-25	
7		, J	001	7	-09-247-3	100
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Jr.	56.6	9.1	1474	4	-08-821-	9
c 10	56.2	0.6	703	4	9-008-813-80-80	Sequence 6, Appli
Ξ	56.2	ئ. د	15.82	Ç,	HS-08-545 1968-10	0
12	56.2		1582	×	US-08-545 196B 12	Sequence 18, Appl
<u>.</u>	56	9.0	1172	- 1	US-07-945-288-9	
14	56	0.6	1172		US-08-462-831 9	
15	56	0.6	1172	_	US-08-461-809-9	5
16	56	0.6	1172	~	US 08:461 441-9	
17	10	0.6	1172	uβ	FCT US93 08518-9	Sequence 7, Applica
c 18	55 6	σ «	5,000	_	ES-07-867-106 2	ru
19	55.4	8.9	1578	4	US-09-416-050A-1	
20	55.4	්. න	1578	4	US-04-664-800-1	Sequence 1, Appli
21			1578	4	US-09-665-309-1	_`
22			3527	C1	US 08-909 9656-7	۲٠
. 23			1534	-	US-08-300-903A-6	ټ
24			1075	₹	US-08-400-0068-6	٠,
и: С1	54.2	8.7	2882	33	US-09-027 137 2	- 4
97		တ <u>.</u> ဆ	1364	7	-08-265-	4
27	53.8	9.8	1364	~	US-08-621-493-3	Sequence 4, Appli

INDIVIDUAL ISOLATE:

3,3	8, 16	4, Appli 4. Appli	8, Appli	l, Appli	<u>`</u>	4, Appli	5, Appli	14, Appl 5258287		30
Sequence	Sequence	Sequence	Sequence 8,	Sednence	Sednence	Sequence	Sequence	Sequence Fatent No.	Sequence 14,	Sednence
US-U8-965-688-3 US-09-260-173-3	US-08-267-803B-8 US-09-041-886-16	US-08-361-467B-4 US-08-484-3326-4	US-08-300-903A-8 US-JB-655-352-10	US-08-242-677-1	8 5 5 0	11S 08 897 340 4	PCT US94 10080 5	US-09-014-969-14 5258287-23	PCT US96-10521 14	US-09-248-335-35
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ALIGNMENTS

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APPLICANT: Prieto, P. A.
APPLICANT: Seo, A. E.-Y.
AFILICANT: LaxLer, J. H.
APPLICANT: Commings, R.D.
TITLE OF INVENTION. Method for Inhibition of Human Retavirus Infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | FELDER APPLICATION | 453 | No. 5575300 applicable | TELECOMMUNICATION INFORMATION: | TELECOMMUNICATION | 12LEPHONE: | (514) 624 374 | TELEX: | No. 5576300e
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 15 Inch, 1.44 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh System 7.1
SOFTWARE: ClarisWorks 1.0
COMPRENT APPLICATION DATA:
APPLICATION NUMBER 185/08/208,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CONA PERCRIPTION: Human milk kappa casein
                                                                                                                                                                                                                                                                    ADDRESSEE: Lounie R. Brayer
ADDRESSEE: ROSS Products Division
                                                                                                                                                                                                                                                                                                         SEE: Abbott Laboratories
: 625 Cleveland Avenue
Columbus
                                       : Sequence 1, Application US/08308883
: Patent No. 5576300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEC ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                           United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 857 base pairs
TYFE: Nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                 APPLICANT: Mukerji, P.
                                                                                                                                                                                                                                                  CHRESFONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                       TITLE OF INVENTION.
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                                                                                GENERAL INFORMATION:
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                   US-08-308-883-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN:
RESULT
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Ob: UNA sequencing and restriction analysis. The encoded product of nucleotide SEU ID NO: 1: is the hu
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OPERATING SYSTEM: MacIntosh System 7.1(D)SOFTWARE: ClarisWorks 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    505 tettiittiaeigagetattiaallittieaattiiteaattiitagatiattiiadigga 564
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67.8%; Pred. No. 0.00029;
Live 0; Mismatches 89; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
DESCRIPTION: Human milk kappa casein
HYPOTHETA'AL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE Soutere: Human Manmary Gland
                                                                APPLICATION NUMBER: US,094,730,163
                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/2009,892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOCUMENT NUMBER: PCT/WOG3/15196
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 624-3774
TELEFAX. (614) 624-3774
TELEX: No. 5712250e
INFORMATION FOR SEU ID No. 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: Adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammary qland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hansson et al
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Best Local Similarity 67.8%
The second similarity 67.8%
Second seco
                                                                                                                                                                                                                                                                                                                                                                                                                                                      857 base pairs
Nucleic acid
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                                     CURRENT APPLICATION DATA:
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IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE: Human
                                                                                                                                 CLASSIFICATION: 435
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PUBLICATION DATE:
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                                                                                                  FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    625 a 625
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                                                                                                                                                                                                                                                                                                                                                                                                                           LOCALION: 45...593

IDENTIFICATION METHOD: DNA sequencing and restriction analysis
OFHER PRORMATION: The encoded product of nucleotide SEU ID NO: 1: is the human
AUTHORS: L. Hansson et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Encoding Kappa Casein, Process for Obtaining the Protein and Use The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Product for Inhibition of Human Potavirus Infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                719 TCHTCHTCHIACATTTTACATHCATGCGCACATFCAAFAFFFFGGTTCHTSCACAATAA 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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67.8%; Pred. No. 0.00024;
tive 0; Mismatches 39; Indels
                                                                                                                                                                                                     MMEDIATE SOURCE: Human Mammary Gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROSS Products Division
Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOCUMENT NUMBER: PCT/W094/15196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION DATE: 05-AUG-1993
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08730163
Patent No. 5712250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            525 Cleveland Avenue
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                                 HAPLOTYPE:
TISSUE IYPE: Mammary atand
CELL TYFE:
   DEVELOPMENTAL STAGE: Adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-1993
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APPLICANT: Prieto, P. A.
APPLICANT: Seo, A. E. Y.
APPLICANT: Baxter, J. H.
APPLICANT: Camminds, R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 82; Conservative
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        CHROMOSOMEZSEGMENT.
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loral Similarity
                                                                                                                                                                                                                                                                                                POSITION IN GENOME:
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                                                                                                                                                                                                                            LIBRARY:
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CITY: C
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Score 58.6; DB 4; Length 857, Pred, No 0 00029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE PATANTIN Release #1.0, Version #1.30 CURPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: IIS/08/256,799
FILING DATE: 06-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Fluppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                US-U8-25b-799-1
: Sequence 1, Application US/08256799
: Patent No 6222044
                                                                                                                                                                                                                                                                                       BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                   HANSSON, Lennart
STROPMOVIST, Mats
RERGSTROEM, Sven
HERNELL, Olle
Toernell, Jan
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REGISTRATION NUMBER: 28 005
REFERENCE/DOCKET NUMBER HAN
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TELEPHONE: 202 628-5197
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nucleic acid
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PRIOR APPLICATION DATA:
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MOLECULE TYPE: CDI
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APPLICANT:
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839 A 839
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9.48, 67.8%;

Query Match Best Local Similarity

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39; Indels
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419 Seventh Street, N.W., Suite 300
∩; Mismatches
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FILING DATE: 05-JUN-1995
PPIOP APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPPATING SYSTEM: PC-1028/MS-DOS
                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/28462437; Patent No. 6232094
; GENERAL INFORMATION:
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FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
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APPLICANT: STROEMQVIST, MALS
APPLICANT: BERGSTROEM, Syen
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TELESAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
82; Conservative
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nucleic acid
EDNESS: single
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45..104
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One Liberty Place 46th Floor
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APPLICANT: Chang, Andy C M
APPLICANT: Williams, Meith L
TITLE OF INVENTION: Mimoved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
                                                                                                                                                                                    Query March 9.4%; Score 58.6; DE 4; Lenath 857; Best Local Similarity 67.8%; Pred. Nc. 0.00629; Matches 82; Conservative 0; Mismatches 39; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: AC EJ 7187
APPLICATION NUMBER: PCT/AU90/00530
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REFERENCE/DOCKET NUMBER: RICE-0002
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FILLING LATE: 19920625
PRIOR APPLICATION DATA:
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Patent No. 5389526
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RECISTRATION NUMBER: 35,134
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INFORMATION FOR SEQ ID NO: 4:
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AFTORNEY/AGENT INFORMATION:
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LENGTH: 4138 base pairs
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TOPOLOGY: circular
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US-07-867-106-4
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                                                                                    NAME/KEY:
                                                                                                      ; LOCATION:
08-462-437:1
                        NAME/KEY:
                                          LOCATION:
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FEATURE
                                                            FEATURE:
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499 atataqtettttttaetgaqetatttaattttaatttteaatttteaeeaataaqaffattta 558
                                                                                                                                                            9.4%; Score 58.2; DB 1; Length 4148;
66.1%; Pred. No. 0.00041;
tive 0; Mismatches 43; Indels 0; Gaps
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Best Local Similarity 56.4%; Pred. No. 0.00069;
Matches 106; Conservative 0; Mismatches 82; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MOCHAEL BELLICANT: MOCHAEL BELLICANT: MOCHAEL BELLICANT: MOCHAEL BELLICANT: O'REBEE, BANKEL BUTLE OF THEWENTON: SOTHEAN GLUTATHIONE-S-TRANSFERASE PUTLE OF THEMSTRON: SOTHEAN GLUTATHIONE SOTHEAN GLUTATHIONE.
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MEDIUM TYPE: DISKETLE, 4.50 INCH
COMPUTER IRM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/924,747
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/08924747
Patent No. 6063570
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IELEPHONE: 302-892-8112
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Ouery Match
Best Local Similarity 66.1%
Merches 84; Conservative
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nucleic acid
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0S-08-924-747-25
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                        1954 AAAAAAA 1948
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COUNTRY: UNITED STATES OF AMERICA
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789 CATAATAAGTAAGTATGATTTTGGGAAACAATTATCTTGTTGTGAGGAAAGGATTGT 848
                                        498 catalagictititiacigagetatilaaliiititeaattiearuutaavaltaliil 557
                                                           438 catcatcagotetgatataaattgeteetaaggagagaaaattetagttgggagaataat 497
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APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE FNZYMES
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APPLICANT: O'KRERE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHTONE-S-TRANSFEBASE
TITLE OF INVENTION: ENZYMES
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ADDRESSEF FIL DU PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: HS/09/247,373B CURRENT FILING DATE: 1999-02-10
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PRIOR FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09247373B
Patent No. 6168954
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SOFTWARE: Microsoft Office 97
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Best Local Similarity 56.4%
Matches 106; Conservative
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56.4%; Pred. No. 0.00069;
tive 0, Mismatches 82, Indels
                                       MEDIUM TYPE: DISKETTE, 3.50 INCH
CUMPUTER: HAM PC COMPATIBLE
COPERATING SYSTEM: MICHOSOFT WORD POP WINDOWS 95
SOFTWAKE: MICHOSOFT WORD VERSION 7.0A
CUMRENT APPLICATION DATA:
AFELICATION NUMBER: US/03/296.715
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FARLIER FILING DATE: 1996-03-22
NUMBER OF SEQ 10 NOS: 89
                                                                                                                                                                                                                                                                                                         REFERENCE/LOCKET NUMBER: CL-1108 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 64, Application US/08821994A ; Patent No. 6228643
                                                                                                                                                                                                                                                            NAME: FLOYD, LINDA AXAMETHY REGISTRATION NUMBER: 33,692
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APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Didier RP
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TITLE OF INVENTION: Promoters
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TELEFAX: 302-773-0164
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TYPE: nucleic acid
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                      COMPUTER READABLE FORM:
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                                                                                                                                                                                      FILING DATE:
19898
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GENERAL INFORMATION:
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                                                                                                                                                       Caps
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                                                                                                                 9.1%; Score 56.6; DB 4, Length 1474;
65.4%; Pred. No. 0.0068;
tive 0: Mismatches 44; Indels 0
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0; Mismatches 43; Indels
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TITLE OF INVENTION: MOLECULES EXPRESSED IN HIPPOCAMPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/313,300 CURRENT FILIND DATE: 1999-05-17 NUMBER OF SEQ ID NES: 15 SOFTWAME: PERI PROFISE 1
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// Patent No. 6080577
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/04313300
Patent No. 6222027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yue, Henry
APPLICANT: Tang, Tom, Y.
APPLICANT: Baughn, Mariah, R.
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Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kaser, Matthew, R. APPLICANT: Lal, Preeti
                                                                                                                  9.18
Best Local Similarity 65.45
Matches 83; Conservative
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                               TYPE: DNA
ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; PUBLICATION INFORMATION: US-09-313-300-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     1418 aaaaaaa 1424
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                                                                                                                                                                                                                                                                                                                       619 Jaaaaan 625
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               LENGTH: 1474
                                                                 US-08-821-954-64
SEO ID NO 64
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DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
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APPLICANT: MELKI, JUDITH
APPLICANT: MUNICH, SANGLD
APPLICANT: MUNICH, SANGLD
TITLE OF INVENTION: SUKVIYAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWARF, KOLASCH AND BIRCH, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 9.0%; Score 56.2; DB 3; Length 1582; Post Local Similarity 65.6%; Prod No. 0.00097; Matches 82; Conservative 0; Mismatches 43; Indels 0;
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APPLICANT: MUNICH, ARNOLD
LITTLE OF INVENTION: SURVIVAL MCTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
                                                                                                          E: BIRCH, STEWARI, KOLASCH AND BIRCH, LLP
PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LIA
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121-110P
                                                                                                                                                                                                                                                                                                                                                                            US/08/545, 196B
                                                                                                                                                                                                                                                                                                                 PC-Dars/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 12, Application US/08545196B
; Patent No. 6080577
; GENEPAL INFORMATION:
                                                                                                                                                                                                                                                                                            IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 21. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                          19-0CT-1995
                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1582 base pairs
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                             ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                       FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER.
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US-08-545-1968-10
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPFRATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                              USA
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                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                   STREET:
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FILING DATE: 13 FEBRUARY 1990
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APPLICANT: Chua, Kaw-Yan
IITLE OF INVENTION: CLONING AND SEQUENCING OF ALLEKGENS FROM
TITLE OF INVENTION: DERMALOPHAGOIDES (HOUSE DUST MILES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.0%; Score 56.2; DB 3; Length 1582;
65.6%; Pred. No. 0.00087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43; Indels
                                                                              PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION CLONING AND SEQUE TITLE OF INVENTION DERMALOPHAGOIDES NUMBER OF SEQUENCES:

ADDRESSEE: LAHUVE & COCKFIELD STREET: 50 STREET; SUITE 510
                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: 18,708,545,195E
FILING DATE: 19-00T-1995
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
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FILING DATE: 19920910
                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPEPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 458.642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 9, Application US/07945288
; Patent No. 5433948
                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,350
                                                                                                                                                                                                                                                                                                                         12:
                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: FARACT, C. J.
                                                                                                                                                                                                                                                                                                                                                             1582 base pairs
                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82; Conservative
                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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COMPUTER READABLE FORM:
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                                                                                                                                                            3.5
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MOLECULE TYPE: CDNA
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                                                                                                                                                            CLASSIFICATION:
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                                                                                SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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998 GIIGEGATETETETAAAGAAAAGACAAFFETTATATGAIFGICAGFAATTTAAAA 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: I CELL EPITOPES OF THE MAJOR ALLERGENS FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.0%; Score 56; DB 1; Length 1172; Best Local Similarity 61.8%; Pred. No. 0.001; Matches 89; Conservative Of Mismatches 55; Indels
ATTORNEY/AGENT INPORMATION:
NAME: MANDRAGOURAS, AMY E.
REFISTRATION UNDRHER: P36,207
REPRENCE/POCKET NUMBER: P16,010CC (IMI-024)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: LAHIVE & COCKFIELD
: 60 STATE STREET, SUITE 510
BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DERMATOPHAGOIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/945,288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JMBER: US 580,655
11 SEPTEMBER 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 458,642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 13 FEBRUARY 1990
ATTORNEY/AGENT (NEW-PWATTON:
NAME: MANDRAGOURAS, NAY E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-462-831-9; Sequence 9, Application US/08462831; Patent No. 5552142
                                                                                                           TELEPASE: (617) 227-7400 TELEPAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARATERISTICS: LENGTH: 1172 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   STRANDEDNESS: single
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FILING DATE: 11 SER
                                                                                                                                                                                                                                 TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CONA
                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 1.,738
US-07-945-288-9
                                                                                                                                                                                                                                                                             Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FITTE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM PITTE OF INVENTION: DEEMATOPHAGOIDES NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                  Guery Match 9.0%; Score 96; 18B 1; Tenqth 1172; Best Local Similarity 61.8%; Pred. No. 0.001; Matches 89; Conservative 0; Mismatches 55; Indels
REFERENCE/LOCKET MOMEDR: 1PG 010CC (IMI 024)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/INSTRUCT NUMBER: IPC 010CC (IMI-024) TELECOMMUNICATION INFORMATION:
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60 STATE STREET, SUITE 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/461,809 FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/945,288
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COMPUTER: 1HM PC COMPATIBLE
OPERATING SYSTEM: PC-DGS/MS-DOS
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MBER: US 458,642
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Patent No. 5770202
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RATION NUMBER: 36,207
                 TELECOMMUNICATION INFORMATION:
                                  TELEPHONE: (617) 227-7400
TELEPAX: (617) 227 5941
INFORMATION FOR SEC ID NC: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : (617) 227 -7400
(617) 227 -5941
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APPLICATION NUMBER:
FILING DATE: 13 FEB
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Molecule TYPE: cbNA
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LOCATION: 1...7
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01.8%; Pred, No. 0.001;
09 0: Mismatches 55; Indels
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Rest Local Similarity 61.8%;
                                      1172 base pairs
                   SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SECTION NOT
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                                                          madeic acid
                                                                                                                  MOLECULE TYPE: CONA
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US-08-461-809-9
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July 22, 2901, 00-54-29 ; Sourch time 113 September 8 (Without alignments) 3472 907 Million coll updates/see
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries Database :

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Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			æ			SUMMARIES	
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U	C1	110 €	17.7		C1	AAF58252	Oligonacleotide L
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Bhalla P, Singh M, Swoboda I, Xu H;

12	Oligonucleotide D2 Oligonucleotide D1 Lily LGC1 prometer Cligonucleotide D1 Oligonucleotide D1 Human prostate can TRIB-ABS3 tumour s	projection	Shuffle vector plud Human secreted pro	Secreted protein g Nucleotide sequenc Clone ssm.pk0067.q Soybean glutathion Soybean type III G Oil seed rape cyst Human cancer assoc	Human ORFX ORF147 Human developmenta Survival motor neu Human survival mot Survival motor neu
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                                                                                                                                                 Location/Qualifiers
                 AAX19927 Standard, INA, 625 BP
                                                                      This Ist numberide sequence.
                                                                                                                                                                                                                                                    97AU-0001184.
97AU-0508233.
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                                                                                                                             Lilium longiflorum.
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25-JUL-1997,
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                                   AAX19927;
       AAX19927
RESULT
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WHIL 1999-142936/12.

Why isolated nucleic acid for, e.g. generating male sterile plants - comprises a nucleolide sequence that allows expression of a transposize gene in acarathre and sperm cells of a plant.

The present sequence encodes the LGCI protein from Lity (Lilium longillorum). The sequence specifically allows expression of the properties of a distribute cell and sperm cells of a plant. Also described arc: (1) a generative and sperm cells of a plant. Also described arc: (1) a generative and sperm cells of a plant. Also described arc: (1) a generative and sperm cells of a plant. Also described arc: (1) a generative and sperm cells of a plant. Also described arc: (1) a generative of a transposase, which is capable of inducing transposition of a transposase gene is expressed facilitating transposition of the promoter, the transposase gene is expressed facilitating transposition of the promoter, the transposase gene is expressed facilitating transposition of the product of produce a product from the plant; and (3) a male sterile plant produced by the method. The male gamete promoter and/or gene is useful for facilitating male gamete specific transposon tagged biants are used to cloue cellain gene in the produced seed content, particularly where pollination stimulates fruit development, and where the lack of fettilisation results in seedless fruit. The nucleic acids enable specific genetic manipulation of the male germ line by generating male sterile plants, and fettilitating male sterile plants, and fettilitating male sterile plants, and fettilitating male sterile plants, and results in seedless fruit. The nucleic acids enable specific genetic manipulation of the male gamete specific transposon tagging.
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12] infatigatinanaaannyoneettanggalgalaaaangtgoaanneattiatu 180 181 gitacccaaaocataactygatigacaategyeggiaaacaagagticgagtiaatita 240 361 gtipaanaalggaqoyontatitinipatqotantottattataaaattoaangtataoidataat 120 61 qqqtaotettaaqeatacaacatquqqqeqqtyqqeqqttttctttqcttqcqttctctt. 120 6] gggtactettaaggealacaacatgayggeggtggetgttttetttgettgettgegtletette |20 Caps 1. genet Fonstoannagasjgfftaagtgjan fonstftaat ngaanand opponie 60 l gecaterceateadeagatttaaqtagaaateeattteattagaaaaagategaaaaa 🖭 241 ataaanaatttqtattqtqcacaalctaatqtcaaaqtttcatqtqacqqcttcatacc 241 ataaaraatttatattatgcacaatctaatgtcaaagtttcatgtgacgggcttratacc 301 accgasocastugatectesestistesgaeescittaqtiganggaegaecsaetgiett 361 groadcaalggagegeetattteteatgelactettgtageatteaagtatgeetgagat 301 accgaaccaatugatootcagattatcagaccacttagtgacggaacgaactgcctt 421 gitteeteeateitileageateateateateatetaaaatigeiteetaagaaaaiitei Ó 169.6%, 300rc 625, 58 26, banath 625, 100.0%; Pred. No. 1.86-97; 0, Indels Mismatches ó Ouery Match Best Local Similarity 109.09 Matches 625, Conservative 9 3

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Nucleic acids containing electron transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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129 teacaaaqooqeartiqooqqatqataaaaaoglgoaacootaoaqatiilatqqilaoooa 188
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genetyping, allowing repeat analyses on
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249 tilgtatigigcacaatolaatgicaaagiliteatgigaeggetlealaceaeegaaen 308
                                                         309. aatagateetranattalooganoorttagiganggaangaangaanggoottgooassaa. 368
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                                    Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
                                                                                    Query Match
Best Local Similarity 0.8%, Pred
Matches 5, Conservative 394,
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Best Local Similarity 0.8%; Pred. No. 8.1e-11;
Matches 5; Conservative 394; Mismatches 218; Indels 0;
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                                                                                   (CLIN-) CLINICAL MICRO SENSORS INC.
                                               20000S-019)259.
                                 9908-0145695
26-JUL-2090; 2000W0-US29476
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Nucleic acids containing election-transfer group, useful as labels in
hybridication assays, e.g. for genotyping, allowing repeat analyses on
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                              AAF58259 standard; DNA; 936 BP
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Nucleic acids containing electron-transfer group, useful as labels in
hybridication assays, e.g. for genetyping, allowing repeat analyses on
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309 aatagatootoottateagaeeaettogfgaogjaaomanatetjesttotsaaaa 268
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                                                                                                                                                                                                                                                                                                                                                                                                      and single-nucleotide polymorphisms, e.g. for genotyping,
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Secret 113 C, 58 22, Length 936,

Query Match Best Loral Similarity 0.8%; Pred. No. 8.1e-11;

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                     429 atettteageatealeagetettgatataaaattgeteetaaggaaqaaattetagee 488
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17-MAR-2000; 2000US-0190259.
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Example 6; Page 127; 159pp; English.
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RESU AAF5 ID XX AC	RESULT 12 AAF58252 1D AAF58252 standard; DNA; 936 BP. XX AC AAF58252;	
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XX PA	(CLIN-) CLINICAL MICRO SENSORS IN:	
X I I	Umek RM;	
DP.	WPI; 2001-159728/16.	
Y	Nucleic acids containing electron-transfer group, useful as labeis in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface	
X S X	Example 6; Page 128, 159pp; English.	
. 2888888	The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions ("ismatches) and single-nucleotide polymorphisms, e.g. for genotyping,	
SO X	Sequence 936 RP; 5 A; 139 C; 10 G; 6 T; 776 **hor;	
On Ma	Owery Match Best Local Similarity 0.8%, Pred. No. 1 310, Matches 5; Conservative 393; Mismatches 219, Indels C; Gaps 0,	
Qy Db	9 atcaacagaaggtitaagtggaaatccailinallagaaaqqafoqqanaaqqifanin 68 	
Oy Db	69 ttaagcatacaacatgaggggggggggttttttttttgcttgc	
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Nucleic acids containing electron transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                            249 iltyiailyytytaacaaltetaalyteaaayiltealyyacyyyeticalaecegaace 308
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189 aarrataariggatigaraatrggrggtaaaqaagagttogaggtoaatttaataaacaa 248
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                                                                                                                                                                       9 atmagnagaagguttaaagtggaaatmutttmuttagaaaagatmganamanen 68
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                                                                                                   17.5%; Score 109.4; DB 22; Length 938;
                                                                                                                                       494; Mismatches 219; Indels
and single-nucleotide polymorphisms, e.g. for genotyping.
                                                    Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
                                                                                                                      Pred. No. 1.3e-10;
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                monitoring gene expression.
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the element, (2) inducing male sterility in a plant by gerably linking a cytoloxic nucleic acid to a promoter, which directs male gamete specific expression to produce a product from the cytotoxic nucleic acid that inactivates or kills male gametes in the plant; and (3) a male sterile plant produced by the method. The male gamete promoter and/or gene is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promoter, the transposase gene is expressed facilitating transposition of
                                                                                                                                                                                                                                                                                                                                                                                                                                    1-neithernm). The sequence specifically allows expression of the queen in generative and sperm cells of a plant. Also described are: (1) a queent construct comprising a generative cell and sperm cell specific promoter operably linked to a transposase, which is capable of inducing transposition of a transposable element such that upon expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               male germ line by generating male sterile plants, and tacilitating male
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The method is useful for producing seedless fruit or fruit with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the product of pollen grains is screened for a range of phenotypes of interest, and the transposon tagged plants are used to clone certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reduced seed content, particularly where pollination stimulates truit development, and where the lack of fertilisation results in seedless
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                                                                                                                                                                                                                                                                                                                                                                                                                 the present sequence represents the LGC1 promoter from Fily (Lilium
                                                                                                                                                                                                                                                                             New isolated nucleic acid tot, e.g. generating male sterile plants comprises a nucleotide sequence that allows expression of a transposase gene in generative and sperm cells of a plant
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Query Match
Best Local Similarity 10.6%; Pred. No. 0.00022;
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Genoscope - Centre National de Sequencage

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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DEFINITION
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/tissue_type="placenta"
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/forte="Vertor: prWSPOPT 6: Site_l: NotI: lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
eloned into the Not I and Pro PV sites of the prWSPOPT 6
vector. Library was normalized library was constructed by
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Mammalia; Eutheria; Primates; Cataribini; Hominidae; Homo.
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47 (%) Fred Mc 0.60067;
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Email: seqref9qenoscope.cus.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/note-"Vector: pCMVSPORT 6; Site_1: Not1: 1st strand cDNA was primed with a Not1-vliqu(dT) primer Five prime end enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV situs of the pGMVSPGRT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies. Contact : Feng Liang Life Technologies a division of Invitrogen 9800 Medical Center Drive
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 329)
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Email: Liangeliletech.com URL:
http://fullengeliletech.com.com.
13-60-t. 67-0thers
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BP 191 91006 EVRY cedex · France
Email: segref @genoscope.cns.fr, Web : www.genoscope.cns.fr.
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43.0%; Pred. No. 0.001;
ntive 47; Mismatches 38; Indels 0;
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Unpublished (2001)
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Fmail: jwatanabemnaqe.ims.u-tokyo.ac.jp
Seruki.Y. Yoshitomc Makaqua.K., Maruyama K., Seyuma.A. and Sugano
.S. Construction and characterization of a full length-enriched and
a 5' end exriched cDNA labrary Gene 200 (1.2), 149 156 (1997).
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AU087256 Sugano Malaria cDNA library Plasmodium falciparum cDNA
Close NFD1288, mENA sequence.
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The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Fai: 81-3-5449-5410
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10.9%; Score 68; DB 105; Length 329; 46.8%; Pred. No. 0.0014; ivo 41; Mismatches 26; Indels (

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was primed with a NoLI-51190(dI) primer. Five prime end enriched, double-stranded cDNA was digested with NoL I and colored into the NoL I and Eco KV sites of the pCMVSPCP1 for vector. Library was normalized. Library was constructed by Life Technologies. Contact. Feng Liang Life Technologies. Contact. Feng Liang Life Technologies. A division of Invitrogen SRG Medical Center Drive Enrich Maryland 18850, USA Eds. (1) 591 CTG 8271 Email: Fliang@lifetech.com URL:

Email: Fliang@lifetech.com URL:

A g g 66 t 15 others
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/note="Vector: pCMVSPORT 6; Site_i. Not1, 1st strand cDNA
                                                                                                                             Homo sapiens
Bukaryota: Motasoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates, Catailhini; Hominidae; Homo.
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1 (bases 1 to 523)
Li.W.E. Gruber.C., Jessee, J. and Polayes, D.
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Location/Qualifiers
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/mote-"Vector removers.
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/mote with a NotL-oilyo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco Rv sieses of the proveper of vector Liberty was normalized, Liberty was constructed by life Technologies.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%; Shope 66.8; DR 105, Length 523; 61.1%; Pred. Mo. 0.0023;
Live 16, Mishatches 33, Indels 0;
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BP 191 91006 EVRY codex - France
Email: seqtetégenoscope - ris fr. Web. www.genoscoge- ris fr
Location/Qualifiers
                                                                                      Score 66.6; DB 105; Length 311;
Pred. No. 0.0025;
2; Mismatches 36; Indels 0;
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/tissue_type="placenta" //issue_type="Vector: pCMVSPORT 6; Site_1: Not1; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with and
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AL515307 LT1_NF1006_PL2 Homo sapiens cDNA clone CL0BB030ZC05 3
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Email : fliang*lifetech.com URL :
http://fulllength.invitrogen.com"
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Location/Qualifiers
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                                                                                                         10.6%; Score 66; UB 105; Length 474; 42.4%; Prcd. No. 0.0032;
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4444 Förest Park Parkway, Box 8501, St. Louis, MO 63108
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/clone_lib="BARC 5BOV"
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                                                                                                                                      Email: tads@lpsi.barc.usda.gov
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/lab_host="NH10B"
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gland cDNA library
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BF 131 91066 EVEY (-dex + FEANCE (F mail - seqrefágencs) gende

    Web : www.genuscope.cms.ft)
    Determination of this RAC-end sequence was carried out as part of a

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                                                                                                                                                                                                                                                                                                                                                                                                              collaboration with the Entopean Drosophila Genome Postpar (FDRP) - http://www.edgp.ebi.ac.uk -. This brosophila Genome Project (FDRP) - library (Dros PAC) was made by Alain Billand at CEPH (Centre d'Frude de Folymerphisme Homain) with funding precided Ly a MEC project grant. The DNA was prepared from embryos by Alain Rocherland Genevieve Payan. It has been constructed in the vector pBeloBAC11.
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Mammalia; Eutheria; Cetartiodactyla, Ruminantia, Pecora, Bovoldea;
                                 CNSO145P 1043 bp DNA GSS 26.7HI-1999
Prosophila relangaster genome survey sequence 17 end of shi
BACN11G11 of DrosbAC library from Drosophila melanogaster (fruit
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Pteryyota, Neopleia, End-pt-rygeta, Dipleta; Brachygera;
Muscomorpha, Ephydroid-a; Irrosophilidae; Irrosophila.
Glassa 1 to 1043)
Genoscope.
Direct Submission
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/plasmid-"pBeloBAC11"
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Single pass sequencing. Bases called and alt_trimmed with phred win 9RA9904 & Vector identified by cross_match with the eminstore 18 and eminmatch 12 options.
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Library made from pooled mENA isolated from mammary
tissous at eight physiological, developmental, and disease
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Marra,M., Hillier,J., Allen,M., Rowles,M., Dietrich,N., Dubuque,T.,
Aspsel,S., Kurahai, Lacy,M., Le,M., Mattur,J., Morris,M.,
Schellenberg,K., Stephen,M., Tan,F., Underwood,K., Moorre,R.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R., and
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Mammalia, Eutheria, Fodentia, Scinnegnathi, Muridae, Murinae, Mus.
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OSEA, ARS, Belusville Agricultural Pesearch Center
Bedg. 200 Em 2A, Belusville, MD 20705, USA
Reiss 1504 8416
Pax: 301 504 8414
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/noie-Torgan: embryo; Vector: pSPORT: Site_1: Noil:
Site_2: Sall, Sized and Directionally from mRRA prepared
from Bob biastocysts.
SitedOptial Conveysts.
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SitedOptial Conveysts.
Colored into the Noil/Sall Sites of a pSPORT vector (Lite
frehmologies). Two different size selections: BI (larger inserts) and 83.
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BOX 510089, 74# Shongshen Er Boad, Gaungzhou, Guanadona, P.K. Dina
                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (into@image.llnl.qov) for further information.
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Eukaryota, Motazoa, Platyhelminthes: Bhulditophora, Newdermata,
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                             /clone_lib-"Knowles Solter mouse blastocyst Bl"
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66.4%; Pred. No. 0.0056;
ative 0; Mismatches 47; indels
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/dev_stage="embryo (pre-implantation)"
/lab_bost="DH108"
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FORWARD: Lambda qtll Forward Primer
                                                                                                                                                                                                                           /organism-"Mus musculus"
Email: mouseest.dwatson.wustl.edu
                                                                                                                         vector to vector length is 725
High quality sequence stup: 192.
                                                                                                                                                                                                                                                      /Strain "B4DC E1/1"
/db_xret="taxon:10090"
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Fax. 86 20 87331679
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Hest Local Similarity 66.4%,
Thus 93, Conservative
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from adult worm, was inserted into the barteriophage lambda qtll Shi-Not arms between Erödt and Notl site of the Lac gene. The chMA library was centracted by Chen St. at Manjina Mcdical Chiresity, Nanjina, Jianasu, P.R. China, (see: Chen Shuzhen, et al. Chinese Johinal of Zvonoses 1977;13(6): 23-25)"
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Noil: Several hundred adult Schistosoma Japonicum(Jiangxi,
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// ISSER_rype "placenta"
/Rote_"Weeter placeNSPORT 6: Site_1: Net1: 1st strand cONA was primed with a NOI 1-01140(dT) primer. Five prime end
                                                                                                                                                                                                                                                                                                                                   P.R.China, strain), of mixed sex, were pertused from the mesenteries of experimentally infected rabbits. Double-strain cDNA synthesized with the mkNA isolated
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                               /strain="Chinese"
/db_atef "tawon-6182"
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//ione="JAYSGUID-GY"
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LLW-B., Grubber C., Jessee, J. and Polayes, D.
Pull-length cDAA, Libraries and normalization
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BP 191-91006 EVRY cedex - France
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cDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL DNA Sequencing by: Washington University denome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
enriched, double-stranded cDNA was digested with Not 1 and
                        clouded into the Not I and Ero RV sites of the pGMVSPORI 6 vertor. Through was naturallized. Library was shall noted by Life Technologies. Contact: Found Liang Life Perhadologies. a division of Invitroach 9800 Medical Center priva-
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similar to TR:Q15004 Q15004 ORF, COMLPETE CDS. ;, mRNA sequence.
A1345131
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Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NOT-CGAP http://www.ncbi.nim.nih.qev/nciedap.
National Cancer Institute, Cancer Genome Anatomy Project (FGAP),
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                                                                                                                       Rockville, Maryland 20850, USA Fax : (1) 301 (10 8371 Email : filang@lifetech.com URL. http://fulllength.invitrogen.com" 14 c 6 g 112 t 8 others
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/tissue_type="invasive_adenocarcinoma"
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Insert Length: 426 Srd Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 316.
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Confact: Robert Strausberg, Ph.D.
Email: cqapbs-r@mail.nih.gov
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/lab_host="DH10B"
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AUTHORS
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Best Lecal Similarity
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Search completed: July 22, 2001, 01:39:52 Job time: 4738 sec

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Copyright (c) 1993 - 2000 compages Ltd.
GenCore version 4.5
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OM protein - protein search, using sw model

July 18, 2001, 17:27:28 ; Search time 12.15 scoonds (without alignments) 212.049 Million cell updates/sec Pyn on.

US = 09 - 463 - 480 - 4Perfect score:

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Jotal number of hits satisfying chosen parameters: 193259 segs, 20144635 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

1: //gni2_6/ptoddia///raa/fa //gnin prp.*
2: /ran2_6/ptoddia/2/jaa/fp COMH prp.*
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Pred. No. is the number of results predicted by chare to be a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

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Result.	Score	Query Match	Length	60	ID	Description
-	75.5	11.0	530	4	US 08 943 714 12	Sequence 12. Appl
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US-08-478-572-4	PCT-US93-08518-4	PC: - US91 - 02166-13	US · 08 - 701 - 240 - 4	US-09-138-236-4	US-08-485-568A-4	US-08-357-698-6	US 68-596 554A-4	US-09-184-223-4	PCT US93 12682 6	US:09-032-315-1	US-08-993-318A-1	US-08-689-421-27	0.5 0.9 3.99 8.86 1	08-09-396-260-1	US-09-389-528-27	US 09 181 827A 27	US-08-816-346-58
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ALIGNMENTS

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E. No. 6187578, No. (187578disk of No. 6187578th America, Inc. 405 Lexington Avenue
                                                                                                                                                          APPLICANT: Klotz, Alan
APPLICANT: Mathisen, Thomas Brik
APPLICANT: Dambmann, Classes And Nucheic Acids
TITLE OF INVENTION: Encoding Same
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSty for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: F.S.ON.9443,714 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4330.200-US
                                                                             APPLICANT: Blinkovsky, Alexander
APPLICANT: Berka, kandy
APPLICANT: Rey, Michael
                     ; Sequence 12, Application US/08943714
; Patent No. 6187578
                                                                                                                       Rey, Michael
Golightly, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIOKNEY/AGENT INFORMATION:
NAME: Lambirs, Filss J
REGISTRATION HUMBER: 3,728
REFERENCE/DOCKET NUMBER: 4990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-9123
TELEPHONE: 212-87H-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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amino acid
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; TOPOLOGY: linear
US-98-943-714-12
                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10174
COMPUTER READABLE FORM:
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                                                              GENERAL INFORMATION:
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STAIE: NY
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US-08-943-714-12
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                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                   New York
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                                                                                                     51 VNLINNLYCAQSNVKVSCD----GLHTTEPIDPHIIRPLSDGTNNCLVNNG----API 100
                                                                                                                             603 MPLVAVIAACVVFCMKRKRKRAQEKDDAEARKONFONAVATMHINGSGVGVALASASLGG 662
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                                   10 CVLPCMVHKAALADDKTCNP------TOFMVTQTTTGLTTGLTTGKVEFE 50
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25, Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                      LILLE OF INVENTION: NOVEL HUMAN DELTAS COMPOSITIONS AND FITLE OF INVENTION: THERAPEUTIC USES THEREFOR NUMBER OF SEQUENCES: 23 ANTICHER ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Indels
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OPERATING SYSTEM: PC-DOS/MS-bus
SOCHWARE Faterfor belease #i G, Version #l 30
CURRENT APPLICATION DATA:
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15; Mismatches
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one Post Office Square
                                                                                                                                                                           101 SHATLVAF-----KYAWDVPPSFSI 120
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                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/U8872855
Patent No. 6121045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Arnold, Beth E. REGISTRATION NUMBER: 35,430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEG ID NO: 11:
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: 514
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT: McCarthy, Sean APPLICANT: Gearing, David TITLE OF INVENTION: NOVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      830 amino acids
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32; Conservative
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COMPUTER READABLE FORM:
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FILING DATE: 11-, THN
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Bost Local Similarity :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boston
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APPLICANT: Artavanis-Tsakonas, S. et al.
TITLE OF INVENTION. Therageuile And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based on No. 5786158ch Proteins And
TITLE OF INVENTION: Uncleic Actds
                                                                                  APPLICANT: Artavanis-Tsakonas, Spyridon et al.
IIILE OF INVENIION: Human No. 5646464ch And Delta, Binding Domains
ITTLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                605 MPLVAVIAACVVPCMKRKRKRAQEKDDAFARQNEQNAVATMHNNSGVGVALASASI.GG 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 KQEFEVNLINNLYCAQSNVKVSCDGLHTTEPIDPHIIRPLSDGTNNCLVNNGAPISHATL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.1%; Score 59; DB 1; Length 833; 24.6%; Pred. No. 12;
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                                                                                                                                                                                                                                                     1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/264,534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FC-DOS/MS-DOS
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Patent No. 5786158
Sequence 6, Application US/98264534
Patent No. 5648464
                                                                                                                                                                                                                             Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1BM PC compatible
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212 464864,9741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,8
PEFFPLINCE,TPYCFET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 24.69
Matches 30; Conservative
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                                                                                                                                                                  NUMBER OF SEQUENCES: 34 CORRESPONDENCE ADDRESS:
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RESULT
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APPLICANT: Rebay, Haria
APPLICANT: Blaumuller, Cristine M.
APPLICANT: Sheford, Scott B.
TITLE OF INVENTION: HIMAN WORDH AND DELIA, BINDING ECMAINS
TITLE OF INVENTION: IN POPORYTHMIC PROPERS, AND METHODS EASED THEREON NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 KOEFEVNLINNLYCAOSNVKVSCDGLHTTEPIDPHIIRPLSDGTMNCLVNWGAFISHATL 105
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                                                                                                                                                                        COMPUTER: IRM PC compatible
OPERATIVE SYSTEM: PC-DCS/MS-FOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Muskavitch, Marc A T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application HS/UR4555UU
Patent No. 5789195
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                                                                                                                                                                                                                                                                                                                     NAME: Misrock, S. Leslie
PEGISTPATION NIMMREP 18,872
                                   Pennie & Edmonds
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                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     833 amino acids
NUMBER OF SEQUENCES: 21
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                CORRESPONDENCE ADDRESS:
                                                                                                                                        COMPUTER READARLE FORM:
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                                                                                      New York
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                                                                     New York
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                                                                                                       COUNTRY:
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APPLICANT: Artavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Ruman No. 584,0869ch And Delta, Rinding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
NUMBER OF SEQUENCES: 30
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                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFIWARE: Patentin Release #1.0, Version #1.30
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
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                                                                                                                                                                                                       PEGISTPATION NUMBEP 18,972
REPERENCE/TWOPET NUMBEP 726-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                ИМВЕК — ПЗ/ОВ/465,500
05-JUN-1995
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FILING DATE: 14-NOV-1991
ATTORNEY/AGENT INFORMATION:
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; Sequence 6, Application 08/08/46126
; Patent No. 5849869
                                                                                                                                                                                                                                                                                                      TELEPAX: (212) 869-8864/9741 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 18, PEFFFFENCE, DUMBER:
                                                                                                                                                                                            NAME: Misrock, S. Leslie
PEGISTPATION NUMBEP: 18.6
  Floppy disk
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                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 833 amino acids
                                                                                CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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                                                                                                       APPLICATION NUMBER-
FILING DATE: 05-JUN
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                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                   CLASSIFICATION:
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MEDIUM TYPE:
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TOPOLOGY:
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us-09-463-480-4.rai

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APPLICANT: Artavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5856441ch And Delta, Binding Pomains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
                                                                                                                                                                                                                                                                                                                                                                                                                             605 MPLVAVIAACVVECMKEKERRAGEKDDAEARKONFONAVATMHINGSGVGVALASASLGG 664
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 67,879,038
FILING LATE: 30-APP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08346128 Patent No. 5856441
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                          : 212 8698864/9741
66141 PENNIE
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66141 PENNIE
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                                                                                     INFORMATION FOR SPQ ID NO: 6:
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amino acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                               ; MOLECULE TYPE: protein
US-08-346-126-6
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                       TELEPHONE:
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                                               TELEFAX:
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TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based on No. 6083904ch Proteins And
TITLE OF INVENTION: Nucleic Acids
                                                                                                                                                                                                       46 KQEFEVNLINNLYCAQSNVKVSCDGLHTTEPTDPH111RPLSDGTNNCLVNNGAP1SHATL 105
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                                                 34; Gaps
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                                                                                            1 MRAVAVFFACVLFCMVHKAALADDK -------TCNPTDFMVTUTTTGLTTGG 45
Query Match
Best Local Similarity 24.6%; Pred. No. 12;
Matches 30; Conservative 15; Mismarches 43; Indels
matches 70; Conservative 15; Mismarches 43; Indels
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/083,590
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PS/08532384 Patent No. 6083904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pennie & Edmonds
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IBM PC, compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18,872
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66141 PENNIE
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ATTORNEY/AGENT INFORMATION:
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PEGISTRATION NUMBER: 18,6
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US-08-532-384-2
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MEDIUM TYPE: Floppy
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Best Local Similarity
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APPLICANT: Blaumueller, Cristine M.
APPLICANT: Shepard, Seet B
TITLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DEMAINS
TITLE OF INVENTION: IN TOPORYTHMIC PROTEINS, AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    605 MPLVAVIAACVVFCMKKKKKRRAQEKDDAEARKQNEQNAVATMHHNGSGVGVALASASLGG 664
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                                                 SHELLS | SHESSION | SH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Muskavitch, Marc A.T.
APPLICANT: Fehon, Richard G.
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SYSTEM: PC-DOS/MS-DOS
                                                          - 103N301 - 103N301 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08893828
Patent No. 6090922
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TELECOMMUNICATION: INFORMATION:
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PESISTPATION NUMBER: 18,872
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202 PHOLSCHOTHSSWWOTHGEPROPERCAVALCEPINE --- OCSDGNOTHGSPOODRE 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 FACYLECMVHKAALAD-----DK-----TONPTDFMVFQT1TGLT1GGKQEF--- 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVALIBALIZAQSIVKVSCDGLHTTEFTBETTF-----RPLSD-----G 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.9%; Score 68; DB 1; Length 356; Bost Local Similarity 24.7%; Fred. No. 5; Matches 38; Conservative 13: Mismatches 57; Indels
                                                                         APPLICANT: Attie, Alan D
APPLICANT: Sturley, Stephen L
APPLICANT: Gretch, Daniel G
TITLE OF INVENTION: Soluble LDL Receptor and Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                              OPPEATING SYSTEM: PC-POS/MS-POS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/08/229,162
                                                                                                                                                                                                                        ADDRESSEE: Nicholas J. Scay, Quarles & Brady
STREET: P.C. Box 2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 THMSLVHNSAPISHATLVAFKYAWDVPPSFSIIS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,403
FILLING DATE: 03-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENEFAL INFORMATION:
APPLICANT: ROBINSTEIN, Menachem APPLICANT: NOVICK, Daniela APPLICANT: TAL, Nathan
Sequence 2, Application US/08228162
Patent No. 5721071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application (8/08092817
Fatent No. 5496926
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILLING DATE: 03-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FOR) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Scay, Nicholas J
REGISTRATION NUMBER: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-228-162-2
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                                                                                                                                                                                                                                                                                                                                               ZIP: 53701-2113
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                             GENERAL INFORMATION:
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                                 1071
                                                                                                                                                                                                                                                                                                                           USA
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259 YDCKDMSDEVGCVNVTLCEGPN-KFKC---HSGECTTLDKVCNMARDCKDWSDEPIKECG 314
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Best Local Similarity 24.7%; Pred. No. 16;
Matches 38; Conservative 13; Mismatches 57; Indels 46; Gaps
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PERLICANT: Lomontt, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
TITLE OF INVENTION: OI a Selected Substance Into Gells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSPY: Hamilton, Krock, Saith & Royneids, rof
STREET: Two Militia Drive
                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.5, Version #1.25 CURRENT APPLICATION DATA:
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                      419 Seventh Street, Suite 300
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/092,817 FILING DAFE: 19-JUL-1993
                                                                                                                                                                                    COMPUTER: 1BM PC COMPATIBLE OPERATING SYSTEM: PC-DGS/MS-DGS
                                                                                                                                                                                                                                                                                                                     FILING DATE: 17 JOL 1933
CLASS FECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1L 100696
FILING DATE: 19-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1L 102915
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BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: FU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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INFORMATION FOR SEQ ID NO: 4:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOWNSEND, G. Kevin
                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      860 amino acids
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US-08-092-817-4
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CORRESPONDENCE ADDRESS:
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                                            Washington
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                                                                                              USA
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ADDRESSEE:
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                                                                                           COUNTRY:
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                                                                     STATE:
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202 PHOLESGECHHSSWPCDGGPPCKDKENGAVATCRPDREF--OCSPONCTHUSPQODRF 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 FACVLFCMVHKAALAD-----DK----TCNPTDFMVTQT1FGLT1GGKQEF--- 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHIMERIC PROTEINS FOR USE IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Indels 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 98; Score 68; DB 2; Length 1074;
24.78; Pred. No. 22;
                                                             Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 24.7%; Pred. No. 22;
Matches 38; Conservative 13; Mismatches
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                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPAX: 617-861-9540
                                                                                                    05/08/470,058
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225 Franklin Street
                   COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-D6S/MS-D6S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Heartlein, Michael W. APPLICANT: Lemontt, Jeffrey F. APPLICANT: Concino, Michael F.
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Patent No. 6027921
                                                                                                                                                                                                            32,227
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Granaban, Patricia
Floppy disk
                                                                                                                        06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                          1074 amino acids
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                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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                                                                                                                                                                                                         RECIETRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECHIF TYPE: protein
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                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                              CLASSIFICATION:
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                                                                                                                      FILING DATE:
  MEDIUM TYPE:
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                                                               SOFTWARE:
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330 Hadibēdēbii.Mudābā
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TILLE OF INVENTION: Chimeric Proteins For Use in Transport
TILLE OF INVENTION: of a Selected Substance into Cells
                                                                                                                                                                                                                                                                                              Overy Match 9.9%; Score 68; DB 3; Length 1074; Best Local Similarity 24.7%; Pred. No. 22; Matches 38; Conservative 13; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ALPRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
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                  3 45 5 40 UJ 45 5 6 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08470058 Patent No. 5817789
REGISTRALLON NUMBER: 34,819
            REFEPENCE TO STATE STATES TO THE TELECOMMUNICATION INFORMATION:
TELECHERE: 617/642 : 6770
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                                                                                              INFORMATION FOR SEQ 1D NO: 2:
                                                                                                                                                          1074 amino acids
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MEDIUM TYPF: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                       617/542-8906
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US-08-470-058-4
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Jarit; 24.7%: Fred. No. 32:
Conservative 13: Mismatches 57: Indels 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFELFANT: Lement, Jeffrey F.
APPLICANT: Concline, Michael F.
TITLE OF INVENTION: CHIMBEL PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SHLECTED SUBSTANCE INTO CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Indels 46; Gaps
                                                                                     8 PACVIFCMVHKAALAD------PK-----TGNOTDFMVTQT(TGLFIGGKQEF--- 49
                                                                                                                                                                             50 ------EVNLINNLYCAQSNVKVSCDGLHTTEPTDPHTI------RPLSD-----G 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                   89 INMCLVNACAPISHATLVAFKYAWDVPPSFSIIS 122
                                                                                                                                                                                                                                                                                                           315 THECLININGGOSHVCNDEKIGYEGLGPDGFQLVA 348
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225 Franklin Street
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APPLICANT: Heartlein, Michael W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fraser, Ph.D., J.D., J
REGISTRATION NUMBER: 34,819
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OPERATING SYSTEM: Windows95
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TELEPHONE: 617/542-5070
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INFORMATION FOR SEQ ID NO: 4:
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ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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s 38: Conserv
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02119-2804
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    Query Match
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Search completed: July 18, 2001, 17:28:17 Job time: 49 sec

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GenCole version 4.5
Copyright (c) 1993 - 2000 Compagen 113
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protein seanch, using sw model OM protein

July 18, 2001, 17:27:28 : Search time 21.18 Seconds (without alignments) 361 260 Million cell updates/see Run on.

บร-อิจ-463-48อิ-4 สลร

GCL SUNIGOSIISSIMUS 138 1 MPAVAVFFACVLFCMVHKAA

Title: Perfect score: Sequence:

Scoring table.

412676 segs, 60623988 residnes RIOSUM62 Gapop 10.0 , Gapext 0.5 Searched.

412576 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: Հըմնոնինում

Maximum Match 100% Listing first 45 summaries Post processing: Minimum Match 0*

Databas

A_Geneseq_0601 · * 1: /STES8/a/qdafa/a/deneseq/aproposity/AA}/ado page *	 /SIDS8/qcydata/yeneseq/qcneseqp/AA1981.LA1:* 	4: /SIDSB/graydata/geneseq/geneseqp/AAl983 nAj.*	5. /SIBS8/gcydata/yenesey/yeneseyp/AA1984.DAT:*	6: /SIDS8/grgdata/geneseq/geneseqp/AA1985.DAT:*	7: /SIDSA/gcgdata/geneseg/genesegp/AA1986.DAT:*	8: /S1DS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*	9: /SIDSB/gcgdata/geneseq/genesegp/AAlyms.DAT:*	10. /SIDSK/goguata/geneseq/genese-Ip/AAI489 FAI+*	11. /SIDS8/grgdata/geneseg/jenesegp/AA1990.DA1:*	<pre>12: /SIDS8/grgdata/geneseg/genesegp/AA1991.DAT:*</pre>	<pre>13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*</pre>	<pre>14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAI:*</pre>	15 /STDS8/grgdata/genesegygenesegp/AA1994_FA1+*	16. /SIDS8/gogdata/geneseg/genesegp/AA1995 par-*	`.	18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DA1:*	19. /SIDS8/gogdata/geneseg/genesegp/AA1998.uAT.*	20. (STESR/gradut 1/genesed framskyll, AAL (A)	21. /SIDS8/gcgdata/genescq/jenescqp/AA2000.DAI.*	22. /STDS8/gcgdata/genesey/geneseyp/AA2691.DAT.*	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7 113.5 16.6 127 21 AAAC3110952 8 95.5 13.9 70 21 AAG27387 9 95.5 13.9 75 21 AAG17387 10 95 5 13.9 75 21 AAG17396
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AAG23735	AAU23734	AAG23733	AAG49594	AAC49625	AAG49593	AAC49624	AAG49592	AAG49623	AAW93359	AAG16590	AAG15589	AAB15945	AAP94865	AAF07713	AAG33923	AAR28960	AAR47858	AAB49601	AAR47157	AAK47860	AAH7#244	AAW07621	AAWG7522	AAW147hU	AAB18308	AAY79031	AAY13563	AAY08401	AAY22599	AAW×107 c	AAB21876	AAY79654	AAH 11 1 HAA
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ALIGNMENTS

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AAY04129 standard; Frctein; 128 AA. AAY 04 129

AAY04129;

il-IIIN-1999 (first entry)

Lily GGI protein sequence.

(i) p. Lilium Logitierum, 1971, 1945, pett, polita, male, germ line, promoter, sterile, transposase, sperm cell; pollination, seedless fruit; genetic manipulation, gamete, histone.

Lilium longiflorum.

W09905281-A1

04-FEB-1999.

98WO-AUDO587 24-JUL-1998; 9/AU-0001184. 47AF DOD9233. 31-DEC-1997; 25-18[-1447;

(UYME) UNIV MELBOURNE.

Xu H; Bhalla F, Singh M, Swoboda I,

WPU; 1999-142936/12. N-PSDB; AAX19927.

 $\rm Hew$ isolated nucleic acid for, e.g. generating made steribe plants - comprises a nucleotide sequence that allows expression of a

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                                                                        The present sequence represents the LGCI protein from THY (Lillium Indifferum). The sequence specifically allows expression of the quent in quentally and sperm cells of a plant. Also described are: (1) a quentific construct comprising a generally appear ell specific promoter operably linked to a transposses, which is capable of inducing transposition of a transpossable element such that upon expression of the promoter, the transpossable element such that upon expression of the promoter, the transpossable services and individually transpossition of the element (2) inducing male sterility in a plant by specially likeling a cytotoxic nucleic acid to a promoter, which directs male gamete specific expression to produce a product from the cytotoxic nucleic acid that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification, signal transduction pathway, metalvill pathway, hybridisation assay, genetic mapping: gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                         inactivates of Kills male gametes in the plant, and (3) a finise sterile plant produced by the method. The male gamete promoter and/or gene is useful for Incilitating male gametes percently cransposon tagging, where the product of pollen grains is screened for a range of plantygives of interest, and the transposon tagged plants are used to clone certain genes. The method is useful for producing seedbases that of that of that with reduced seed content, particularly where pollination stimulation seedless fruit. The nucleic acids enable specific genetic manipulation of the male gene inc by generating male sterile plants, and facilitating male gamers specific transposon tagging
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transposaso gone in generative and speom cells of a plact
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                                      Claim 4: Fig 1; 64pp; English.
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990S-0123548.
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9908-0159329,
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Friteis identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping; gene expression control, promoter, termination sequence.
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29.8%; Pred. No. 1.9e-05;
ive 14; Mismatches 63; Indels 10; Gaps
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27-AUG-1999;
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Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control; promoter;
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         Protein identification; signal transduction pathway, metabolic pathway, hybridisation assay, jenetic mapping, gene captession cuntail, promoter,
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This invention describes marters acid encoding enkaryotic neutral sphingomyelinase. The products of the invention can be used for the diagnosis and treatment of diseases associated with over- and under expression, or a echancel or firminated or titily of retrieved mentral sphingomyelinase, or disturbances of refel proliferation, cell differentiation and/or apoptosis. The diseases treated are inflammatory processes, cell grawth disturbances, career and/or metabolic disorders.
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990S-0161361,
990S-0161920,
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11-AUG-1997;
15-OCT-1997;
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21-001-1999;
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Protein identification, signal transduction pathway, metabolic pathway, bybridisation ussign practic rappings gray expression measures.
                                                                                                                23 DOKTONPTDEMVTQTITGLITGGKQEFEVNLINNLYGAGSNVKVSCDGLHITEPTDPHTL 82
                                                                         40, Indels 19;
                                               11.5%; Score 78.5; DB 20; Lonath 41v: 29.8%; Pred. No. 1.1; tive 7; Mismatches 40; Indels 19;
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                                                                                                                                                    83 RPLSDGTINN/LVNNGAPISHATLVAFKYAMDVPP 116
                                                                                                                                                                   AAG23745 standard; Protein; 264 AA
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990S-0126785.
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19-APR-
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hybridisation assay, genetic mappina, gene expression control, promoter; termination sequence.
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US-09-463-480-4 Title: Perfect score:

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Scoring table

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Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

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Database

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1	134	19.6	124	C4	T04636	hypothetical prote
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### ALIGNMENTS

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hypothetical protein Flun7.100 - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 23.Apr.1999 #sequence_revision 23 Apr 1999 #text_change 21 May-1999

C, Accession: T04636
R; Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, Submitted to the Protein Sequence Database, March 1999
A, Reference number: 215263
A, Accession: T04636

A, Molecule type: DNA

A; Fesidues, 1 124 (BEV)

A;Cross-references· EMPL:ALØ21636 A;Experimental source: cultivar Columbia; BAC clone F10N7

C; Genetics:

A;Map position: 4 A;Introns: 20/1

A; Note: F10N7, 100

19 68, Score 134, DB 2, Length 124; 29.9%; Pred. No. 9.1e-07; 60; Indels 29.9%; Pred. .... 38; Conservative Local Similarity Querry Mittel. Matches

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3. AVAVELACVIJECMY - HKAALADDKTCNPTDEMVTQTITGLITGEGEGEFBVNLINNLYCAQ 61.

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62 SNVKVSCFGGLHTTEPTPPHTTPPLSFGTNNCLVNNGAPTSHATLVAFKYAWDVFFSFSII 121 ã

59 KHVTLSCGGFAPAKPVKPLLLQPQG---NTCLMIKGAALPAGATAQFTYAGQ-PYIFRPV 114 Db

122 SEDINCE 128 ö

115 GSKVDPS 121

#### REBULI

T04635

hyperbolical protein F10N7 40 - Atabidopsis thaliana C.Species. Arabidopsis thaliana C.Species. Arabidopsis thaliana (mouse-ear cress)
C.Outer 23 Apr 1999 #sequence_revision 23 Apr 1999 #text_change 21 May 1999
C.Outer 31 Apr 1999 #sequence_revision 23 Apr 1999 #text_change 21 May 1999
E.Marcia, M. Foss, M. Eiser, M. Foss, M. Fibrian, K.D., Hadelsei, T., Mowes, H.W., Mayer, K. Submitted to the Endean Sequence Estabase, March 1999
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Princologis, A.; Ecker, J.K.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chora, M.K.; Conn. L.; Conway, A.E.; Conway, A.E.; Croway, A.E.; Greasy, 1.H.; Dewar, ansen, N.E.; Hudhes, B.; Hudrar, L.
Nature 408, 816-820, 2000
A.Authers: Banter, I.; T. Jun, Y.; Lin, X.; Liu, S.; Fhaykin, F.; Fin, A.Authers: Banter, I.; J.H.; Di, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Euros, J.S.; Maith, R.; Maith, R.
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C)Accession: A86191
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                                                                                                                                                                                                                                                                  164 CSLINSLSVKOSKTGKLVQNKPEWEVRVTNPCNN CKPQNTFLLCVGFNSVTPIDTSLLL 221
                                                                                                                                                  27 CNPTDFMVTQTITGLTIGGKQEFEV---NLINNLYCAQSNVKVSCTGLHTTEPTDPH11R 84
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             Matches 43; Conservative 13; Mismatches 50; Indels
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C.Species: Aspergillus miger
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Nature 402, 769-777, 1999
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submitted to the Protein Sequence Database, March 1999
A;Reference compare 21523
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AJRETETETE number: A85001; MOID:20083488
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Aptrose references: GH:NC_0012FB: NIE:97270115; PIBN:CAB79929:11, GTT B.GN98110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cispecties: Alabidopsis thatling (manse our coust)
Cibate: 16 Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CiSpecies: Arabidopsis thaliana (mouscear cross)
CiDate: 24 Apr 1999 #sequence_registor 23 Apr 1999 #text_change 21 May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 CSLNSLSVKOSKTGKLVQNKPEWEVTNFCNN+++CKFONTELLCVCFNSVTP1DFSLLL_ 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 VTQTTFGLFTGGKQEFEVNLINNLYCAGSNVKVSGDGLHTTEPTDPHLIRPLSDGTNNCL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 VLOSK PANWYENK PEWEVKULNSSWYFTHTTT STYPPFKTYTPTT FILE OF THE THE TELEFOLIST STREET STYPPFKTYTPTT STYPPFKTYTPT STYPPFKTY STYPFKTY STYPPFKTY STYPPFKTY STYPPFK
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                                                                                                                                                                                                                                                                                                                          18.8%; Score 129; DH 2; Length 123;
31.6%; Pred, No. 30-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein A14432110 [imported] - Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Mismatches 42; Indels
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Pred. No. 2.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 VANGAPISHATLVAFKYAWDVPPSFSITSSDINCS 128
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A;Note: F10N7.80
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Aymoleoule type: DNA
A;Residues: 1-26 + 4BEV.
A;Cross-reterences: EMHL:ALO21636
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Rest Local Similarity 31,7%
Matches 34, Conservative
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A:Map position: 4
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                                                              A:Introns: 22/1
A:Note: F10N7.50
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C;Keywords: hydrolase
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A, Residues: 1:23
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Superfamily, serine carboxypeptidase
C) Reywords: glycoprotoin hydrolase; serine carboxypeptidase, sympan
E)1-23/nomain; signal sequence #status predicted <SIG>
E)24-52/Nomain; propertide #status predicted <SIG>
E)23-53/Promain: propertide #status predicted <SIG>
E)23-53/Promain: propertide #status predicted <SIG>
E)23-53/Promain: propertide #status experimental <ANI
E)23-23/Promain: propertide #status experimental <ANI
E)21-43/E)23/231-341/Distailide bonds: #status experimental
E)21-427/506/Active site. Ser. Asp, His #status predicted
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                                                                                 A:Molecule type: protein
A:Residues: 53-94,717,96-113,717,115-129,78Loens7,136-279,75L7,282-322,727,324,747,326-5
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A/Recession: T38371
A/Status, pieliminary: translated from GB/EMBL/D0BJ
A/Rocelle type: DNA
A/Rocelle type: DNA
A/Rocelle type: DNA
A/Rocelle type: A/Rocelle type: DNA
A/Rocelle t
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C.Species: Schizosaccharomyces pombe
C.Date - 01-be: 1999 #sequence_revision Uniter 1999 #text_change partmarings
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C.Date. 16-Jul-1999 #septence_revision i6-Jul-1999 #text_chappe 29-col-1999
C.Accession: Til614; S62448
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R;Skelton, J.; Churcher, C M , Barrell, R G ; Bajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, Pebruary 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53, Indels 37,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 VALINALYCAQSAVKVSCD-----GLHTTEPIDPHITRFLSDGTNACLVAKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%; Score 75.5; DB 1; Length 530; 21.8%; Pred. No. 5.5; Live 25; Mismatches 53; Indule 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.9%; Score 75; DB 2; Length 922; 30.4%; Pred No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32, indept
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 QIESEMSKRVQATAPTS--SLEHFKQLSPISPSFTSSANSIN 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismutches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 SHATLVAF-----KYAWDVFFSFSI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 INGTLLSIQNMTWNGKLGFDTAPSTPI 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٠.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 21.88 Matches 32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                      A; Introns: 67/1; 161/3; 237/2
A; Reference number: S78071
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Matches 31, Conserve
                                               A:Accession: S78071
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                                                                                                                                                                                                                           A:Gene: pepF
                                                                                                                                                                                3; Genetics:
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F. Biatther, F.E.; Ilunkett III, G., Bloch, C.A., Perna, N.I., Buriand, V., Kiley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Chossarpeterions and Alemages, and minimary bits $1298 2869, F103 AND install, F10.3 d882
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession, Stid48
A,Status: preliminary
A,Mulecule type: DBA
A,Residues: 1-1115 <BAD>
A,Residues: 1-1115 <BAD>
A,Cross-references: EMRL,Z54328; NIU-g1009451; PIDN-CAA91128.1; PID-g1009454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 RSMITLYSCEL-CSEHAVLISEESPOIDYBAMFYQSENNFEVVIGGYHQ-KLTVVNABRG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RAVAVEFACVLFCMVHKAALADDKTCNPTDFMVTQTTTG--LFTGGKQEFEVNLIN---- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------NLYCAQSNVKVSCDGLHTTEPI--DPHIIRPLS------DGTNN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 TITGLTIGGKQE-FEVNLINNLYCAQSNVKVSCDGLHTTEPIDPHIIRPLSDGTNNCLVN 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.9%; Score 74.5; DB 2; Length 1115; 21.1%; Pred. No. 17;
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A;Status: nucleic acid sequence not shown; translation not shown
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29.2%; Pred. No #0;
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A;Peference number: A64720; MHID:97426617
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C,K-ywerds, nacteolide binding, Flosp, transmembrane protein
F)54-70/Domain: transmembrane #status predicted <TMM>
R:Barrell, B G.: Rajandream, M.A.; Walsh, S.V.; Wood, V. Submitted to the EMBL Data Library, october 1995
A;Reference number: 217300
A;Accession: T11614
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Recioule type: DNA
A;Residues: 11115 *BAR>
A;Residues: 11115 *BAR>
A;Residues: EMHL/SA43M; NID:glonw454; PID:glonw454
A;Exprimental Scarce: ELLLiu 972h(*)
R;Baddcock, K; Churcher, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable membrane protein b1978 - Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL bata Library, october 1995
A;Reference number: 862445
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A:Map position: IL
A ferrora - 679, (974, 96/2) 164/10, (97/2) 793/1
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Finally, S.T., Brossh, F., Parkhill, T., Garnier, T., Churcher, C., Harris, D., Gordon, Rajandream, M.A., Royels, B., Devlin, K., Peltwell, T., Gentlos, S., Hamlin, N., Holroyd, Rajandream, M.A., Royels, J., Rutlet, S., Seeger, K., Skelton, S., Shuares, S., Nature 393, 537-54, 1998
A.Authors: Sqares, P., Sujsron, T.P., Haylor, K., Whithhead, S., Shuares, S., A., Athier Deciphering the biology of Mycobacterium tuberculosis trom the complete qeno A. Reference number: A70209
A. Accession: A7029
A. Residues: Peliminary, nucleic acid sequence not shown: translation not shown A. Moloculo type: DNA
A. Residues: 1-583 <COL>
A. Residues: 1-583 <COL>
A. Residues: GB:27.250; GB:ALLis455; NID:99251617; PIDN:CAHOLOGG 1; PID-25531
A. Residues: Colored acid sequence of Scoles acid Scoles acid sequence of Scoles acid Scoles ac
                                                                                                                                                                                                                                                                           E. Merihaist, F. J. Leawas, Mar. R. Terchemin, D. J. Hur, F. Mowes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, April 2000
A; Reference number: 224484
A; Accession: 148096
A; Status: profilminary
A; Molecule type: DNA
A; Residues: 1-1261 :CBE:
A; Crass.references: EMBL:Ail63816
A; Experimental source: cultivar Columbia; BAC clone #20010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52/2 34/32 885/3 42/1 4/5/4 161/2 134/3 138/3 139/3
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C;Species: Mycobacterium tuberculosis
C;Arts: 17 Jul 1930 *sequence_regision 17 Tul (1940 #frx/_change 22-0v4-1040
E;Accession: A70729
E;Acolo, S T , Brosch, P , Parkhill, I : Carniar T , Churcher C , United (1970)
                                                                                                                                                                                                  C.Species: Arabidopsis thaliana (mouse ear cress)
C.Dat. 200 Apr. 2000 Banguener_trecision 200Apr. 2000
C.Recession: T48096
E.Checession: T48096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   496 PSTERMSPSVACVQTVGDPQTAVNFHENEFTMITIDDEVTRAQSN···QLSSIVETEARVDF 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462 NEPANVMCADTDGEVICVDERFTFVPSKGFGLLPPTVTPPGLLRFELFFTDNAL----PP_517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FERMILINALYCACHRAVENSCHOLHTTEPIDPH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 NLINNLYCAQSNVKVSCDGLHTT-------EPI--DPHIIRPLSDGTNNCLVNNGAP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 11RPLSD--GTNNCLVNNGAPI----SHATLVAFKYAWDVPPSFSIISSDINGS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           553 VVQGCSEESQTGNCLISETDPIDIQCSHQS-----EKHETPLNPDIVDSSANKS 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.5%; Score 72, DB 2; Longth 1261; 27.2%; Pred. No. 36; Live 16; Mismatches 45; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.4\%; Score 71: DB 2; Length 584; Best Loral Similarity 29 0%; Prod No. 18; Matches 27; Conservative 13; Mismatches 31; Indels
                                                                                                                                                        hypothetical protein 120010.170 - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 ISHATLVAFKYA-----WDVPPSFSIISSDIN 126
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Matches 31, Conservo
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A. Introns 41, 3. 67
A:Note: T20010 170
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C.Accession: E85822
R.Perna, N.T.; Plunkett III. G.: Burland, V.; Man, B.; Glasner, J.D.: Rose, D.J.: Mayhew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A) Residues: 1.2660 (SP).
A)Cross-reference of Apper174, Min 312516151, PIDA AA357511 | SPITA TYON145 TWGF 131
A)Experimental source: strain 0157:H7, substrain PD1933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iller, L.; Grotheck, E.J., Davis, N.W.; Lum, A.; Dimaianta, m.; Potamousts, N.; Apodáca, Natur, 409, 529-533, 2001
Nature, 409, 529-533, 2001
Affille: Genome sequence of enterohemorrhagic Escherichia coli 5157:47.
A;Reference number, A85480, MGID.21674935, PMID.11205551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribietrich, F.S.
submitted to the BMBL Data Library, July 1995
Prescription: The sequence of S. cerevisiae cosmids 9481, 9599, 9926, 9461, and lambda
A;Reference number: S69665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Cross-references: EMBL:H3z274; NIP-g*z7414; FID-gz1441+z: ASPBA-ANDFORT MIPS:YDR*46W
C)Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1838 TVTASMAGGKSEQLVVNFIADTLTAQVNLNVTEDNFIANNVCMTRLQATVTFGNGNPLAN 1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CiSpecies: Saccharomyces cerevisiae
CiDate: 22 Ang 1996 #sequence_revisies 96-sep-1996 #fext_ebange 29-661-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: ::1 1 ::1 1 : :1: : :1: : :145
97 SSSALITCSG----AMVFLASLSAISEAIEDRIIMNSMPELMMISLASLVNIK----- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 QSNVKVSCLGLHTTEPIDPHIIRPLSEGINNCLVNNGAP----ISHATLVAFKYAWDVFP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 TITGITIGGKQF-FFVNIJINIYGAQSNVKVSGTGLHITEPIDPHIIRPLSEGINNGLVN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 VLFCMVHKAALADDKTCNPT----DFMVTQTITGL/TIGGKQEF----EVNLINNL/PCA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 ILLMONIJDIJDGINNSSGGRSSSSFFPPIFINIESI VSFTFWFFI KFNNI SSKNDINSI YSN DA
                                                                                                                                                                                                                                                      probable invasin 22127 [Saported] - Excherichia sali (striin 2122 HZ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
10.6%; Secro 72.5; DB 2; Length 166;
Best Local Similarity 23.5%; Pred. No. 2.8;
Matches 31; Chesevative 24; Mismatches 52; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%; Score 73, DB 2; Length 2669, 29.2%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein YDR396w · yeast (Saccharomyses peremisiae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44, 17,36,37
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C;Superfamily: Saccharomyces hypothetical protein YDR396w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1898 EA-----VTFTLPADVSASFTLGGGGSAITDIN 1925
"1621 EA-----VTFTLPADVSASFTLGQGGSAITDIN 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 NGAPISHATLVAFKYAWDVPPSFSI----ISSDIN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guery Match 10.78 Best Loral Similarit, 29.28 Matches 28; Conservative
                                                                                                                                                                                                                                                                                                     "; Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 SFSIISSDINGS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 SWSSISDIFFCT 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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A;Molecule type: DNA
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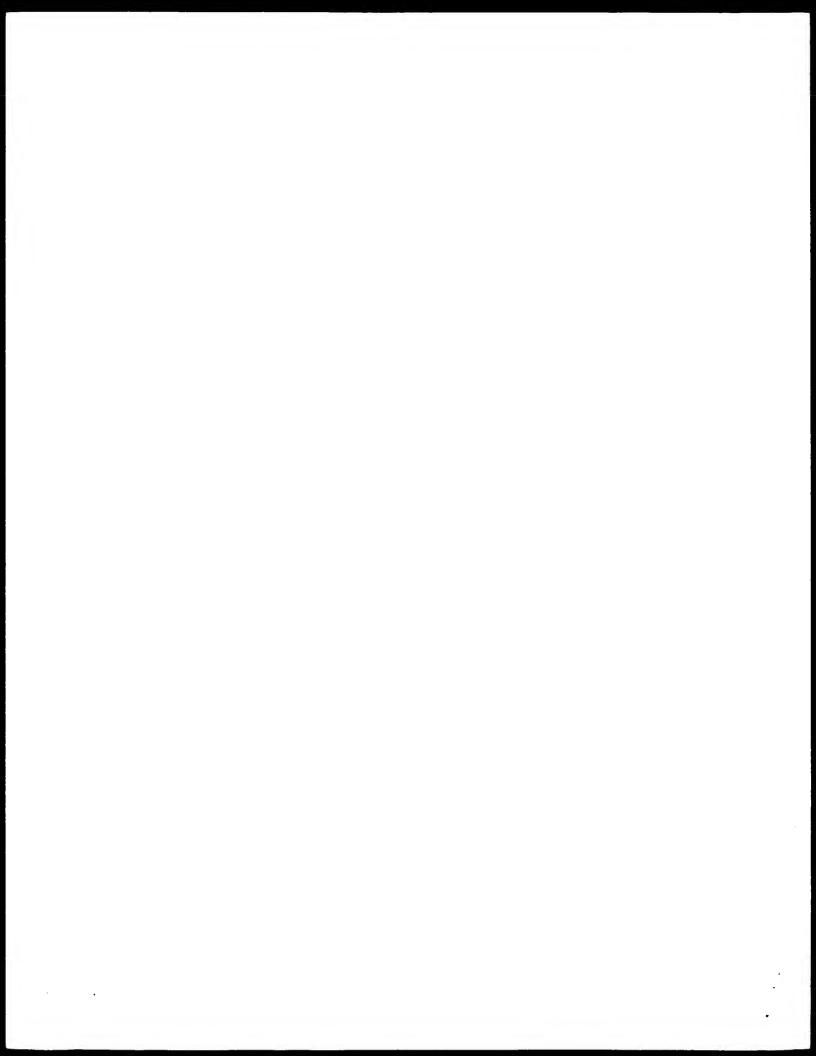
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F,84,177,405,2276,2478,2454,2481,2564,2670,2763,2836,3088,3179,3384,3432,3628,3772,40
98,11066,11488,11615,11635,11949,12170,12478,12526,12645,12875,13803,13836,13835,3354
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.21990,21935,22295,22495,225627,22897,23624,23318,23881,24612,24177,24290,24447,24642,
F:26171,26178,26181,26190,7816dirq site: phosphate (Ser) (ordicat) *status kxperiment
Appearantion: structural protein forming filaments in striated muscle cisupertamily: Litin; fibromectin type III repeat homology; immunoglobulin homology; cisupertamily: Litin; fibromectin reference in reference of mandulin binding, cardiac muscle; duplication; gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Title: Delta, a Drosophila neurogenie genē, is transcriptionally complex and encode
A;keference number: A31245; MOID:89196890
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Geneg Per. 2, 1723-1735, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ncurogenic protein Actu precusor truit fly (presophila melanogaster)
C;Species: Drosophila melanogaster
C;pate: 31-Mar-1990 #sequence_revision 31-Mar-1996 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9567 RQCINERIWERLQPTVEDLIVECTEYEPRVKAVNAAGVSKDSATVOPODYGPPDMPPSIDLE 96.26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.5 MPLVAVIAA:VVECMKEKEKEAQEKDNAEAFKQNEQNAVAIMHINGSAVGVALASASMGG 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 KICHITDEMVTU TITGITHOURGEPEVNIJNNIYCAGENVKVS-CDOLHITEP--IDPH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRAVAVFFACULFCMVHKAALADDK - - - - - - - - TCNPTDEMVTQTITGLTIGG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.4%, Score 71, DB 1, Longth 26926; 29.2%; Prod. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 70; DB 2; Length 832;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ls, Mismatiches
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E,457-488/Pontain: EDF homology
E:533-554/Pomain: EGF bomology
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A,Residues: 1-832 KeP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A 1246
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                                                                                                                                                                                                                                               structural protein
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A, Reference number: A66201; PDB:1NCT
A;Contents: annotation; conformation by (1)H-NMR, residues 'S',26059-26155
                          titin, cardiac muscle [validated] - human
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A.Accession: SASMAS
A.Status: nucleic acid sequence not shown
A.Kolecule type: DNA
A.Residues: 26729 20825 -KCUD
A.Cross-references: EMBLIX52412; NID:q1236751
EMBO J. 12, 3827-3834, 1993
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34, Caps

43, Indels



# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein - protein search, using sw model

Fun on:

July 18, 2001, 17:27:28 ; Scurrh time 11.07 Seconds (Without allymments) 375:724 Million rel: gfates;see

Feriect score: Sequence:

US-09-463-480-4 685 1 MRAVAVEFACVLFOMVHKAA......KYAMDVPPSFSTLSSDENGS 128

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 segs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Mirjmum Match 100% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database ·

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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7	67	- 1	617		FXK1_MOUSE	_
80	67	8.6	648		TKT_MYCPN	P75611 mycoplasma
6	66.5		216	-	OSD4_BUMAN	
10	99	9.6	146		DER2_DERPT	P49278 dermatophaq
11	9	6	276		PLPR_PASHA	3
12	99		531		PEPF_ASPNG	
13	99		662	-	DCHS_HUMAN	
14	65		25.5	, <b>4</b>	E13B_SOYBW	
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16	65		828	-	ENV_HV2RO	
17	65	6.5	1186	_	CEAA_BACTS	
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20	64 5	J D	86.3	П	LDVR_CHICK	
21	6.4 5	ত	1664	-	SLP1_C1OTM	çükş52 elestridium
22	64	9.3	951	-	HEX_ADE05	PO4144 human adeno
23	64	~ 5	1465	٦	AT7B_HUMAN	
24	63.5	9.3	407	_	AK2_BACST	P53553 bacillus st
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P15499 mus musculu	084367 chlamydia t	Ogxta3 bos taurus	P23738 mus musculu	P46103 plasmodium	P53590 sus scrofa	P18477 actinomyces	P33235 escherichia	Q38042 bacteriopha	Pittel Aus musculu	P47312 mycoplasma	P21657 saccharomyc
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                                                                                                                                                                                                                                                                                                                                                                                                                 the Barapean Historicalist Institute. There are no restrict in the cuse by non-profit institutions as bond as its content is in no modified and this statement is not removed. Usage by and for commerce on thirds a profit of an increase of contines (2^{10} + 1)^{1/2} was its force or send an email to licensee(sb-sib ch).
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RADARIN G.C., Worthand J.R., Vandell M.D., Zhang O., Chon L.X.,

Sutton G.G., Worthand J.R., Vandell M.D., Zhang O., Chon L.X.,

RADARIN J.E., Roylo C., Baxter E.C., Holl G., Nelson C. R., Mivlos G.L.G.,

RADARIL J.E., Roylo C., Baxter E.C., Holl G., Nelson C. R., Mivlos G.L.G.,

RADARIL J.E., Roylo C., Baxter E.C., Holl G., Nelson C. R., Mivlos G.L.G.,

RADARIL J.E., Holl R. R., Roylo C., Bandell D., Holskieben S.,

Radassa R.Y., Bences P.V., Retner R.P., Addrew D., Holdin D.,

Rade Bablos B., Doldin D.A., Bulleo C., Pyrchitaroqui U., Roylo C., Bandel S.,

RADARIS R., Doug L.E., Downes M.D., Down J.D., Dow J., Diet Z. M.,

Boston C., Gabriellan M.E., Bownes J., Holskieh P., Holtick P.,

RADARIS R., Doug L.E., Downes M.D., Down J., Diet Z. M.,

Boston C., Gabriellan A.E., Garq N.S., Gelbart W.M., Glasson R.,

RADARIS R.L., Harvey D., Helman T.J., Herrandez J.R., Howek J.,

Harris N.L., Harvey D., Homman T.J., Herrandez J.R., Howek M.,

Harris N.L., Harvey D., Homman T.J., Herrandez J.R., Houck M.,

RADARIS E., Kalren G.E., Kratt C., Morinson J.A., Korlenn R.A.,

Adali M., Kalrish E., Karten G.H., Karit C., Morinson J.A., Korlenn R.A.,

Radaszolo N., Putunan G.S., Pan S., Pollard J., Marphy D.M., Marbhy R., Markey D.M., Morther E., Shou H.,

Radaszolo N., Putunan G.S., Pan S., Pollard J., Wall C.,

Radaszolo N., Putunan G.S., Pan S., Pollard J., Wall C.,

Scheelt K., Sendenton C., Singpenn M., Skupski M.P., Smith H.O.,

Radaszolo N., Putunan G.S., Pan S., Pollard J.,

Radaszolo N., Putun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIANE 891968 W. Final For Manager Manager Median Median Manager MEDIANE 891968 W. Alter A.K., Prefetch K., Knob P.J., Maskaritch M.A.T., "Defical a Brosophila neurodenic dene, is transcriptionally complex and encodes a protein related to blood coaquiation factors and epidermal growth factor of vertebrates.";
                                                                                                                                                                                                                                                                                                                         Vaessin H., Bremer K.A., Knust E., Campos-ortead J.A.;
"The neurogenic game Delta of Drosophila melanogaster is expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Knust E., Dietrich U., Tepass D., Bremer K.A., Weigel D., Vaessin H.,
                                       Pterydota; Neoptera, Endopterydota; Diptera; Brachycera; Muscomorpha:
                                                                                                                                                                                                                                                                                                                                                                                                        nearGaenic territories and encodos a putative transmembrane protein with EGF like repeats.";
                                                                                                                                                                                                                                    SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE
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melanogaster, and their relation to neurogenic genes.";
EMBS J. 6:761-766(1987).
Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta:
                                                                          Ephydroidea; Drosophilidae; Drosophila:
NCBL_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE:87218547; PubMed:3107986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN OREGON'R; TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 422-621 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 6:3431-3440(1987)
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between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license disperement (see http://www.st.stb.ch.down.out.ch.) or send an email to licensedisb-sib.ch.
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EGF-LIKE 2.
EGF-LIKE 4.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 8.
EGF-LIKE 8.
                                                                                                                            SURCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: DETECTED IN ALL AREAS WITH NEHOCIENIC
ABILITIES. FOR EXAMPLE THE NEUROSENIC ESTYDEEM AND THE PRIMOSPIA
OF THE SENSE ORGANS. LATER EXPRESSION IS RESTRICTED TO THOSE CELLS
THAT HAVE ANOPTED A NEURAL FATE.
DEVELOPMENTAL STAGE: EXPRESSED HOTE MATERALLY AND TYPE TO THOSE CELLS
PERFESSION IS HIGHEST EARLY IN EMBRYONIC DEVELOPMENT (STAGE 5) AND
PEDIOUS IO A LOW LEVEL DUFINE LARVAL STAGES.
MISCELLANFOUS SERAPATION OF NEUROAL STAGES.
MISCELLANFOUS SERAPATION OF NEUROAL STAGES.
                                                                                                                                                                                                                                                                                                        MISCRELANROUS: NOTCH AND SPREADE MAY INTERACT AT THE PROTEIN LEVEL, IT IS CONCEIVABLE THAT THE SERRATE AND DELTA PPOPELINS MAY COMPETE FOR BINDIN: WITH THE NOTCH PROTEIN.
                                                       Drosophila melanogaster. 7.

Developmont 110:905-914(1990).

-!-FUNCTION: BSSPNTIAL FOR PROPER DIFFERENTIATION OF DATACHER. D. IS PROUTED FOR THE COPPECT SEPARATION OF NEURAL AND EPIDERMAL CELL LINEAGES.
                                                                                                                                                                                                                                                                              DEVELOPMENT IN INSECTS, THIS PROCESS IS UNDER CONTROL OF THE
PAITERN OF TRANSCRIPTION, AND CHARACTERIZATION MEDIUM: 9209.44: PubMed-212847; Heanlin M. Kramatschek E. Campos-Ortega J.A.; The pattern of transcription of the neurogenic gene Helta of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEUROGENIC LOCUS DELIA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE DELIA/SERFATE/JABSED FAMOLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Differentiation, Neurogenesis, Ropeat, Transmembrane,
BGF-like domain, Glycoprotein, Signal,
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InterPro; JPR001881; -.
Pfam; PF01414; DSL; 1.
Pfam; PF005008; EGF; 9.
PROSITE: PS00012; EGF; 9.
PPOSITE: PS01165; EGF2; 9.
PROSITE: PS01187; EGF_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X06289; CAA29617.1; --
EMBL; Y00222; CAA68269.1;
EMBL; AE003725; AAF5557.1; --
EMBL; X05140; CAA28786.1; --
PIR; S00600; S00670;
PIP; A26647; A26637.
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FlyBase; PBgn0000463; Dl.
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InterPro; IPRO00561; -
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                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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Live 15; Mismatches 43; Indels
| PY STMITARITY |
| BY SIMILARITY |
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01-NOV-1995 (Brl. 32, Last sequence update)
01-NEV-1995 (Rel. 32, Last annotation update)
3FF-THETICAL 1800.8 KDA PROTEIN NOS28.2 IN CHROMOSOME 11.
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Matches 30; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIJINE-9223-8109. PubMed 1532908,
MedijiNE-9223-8109. PubMed 1532908,
Modaira K -1. Nakano K. Ckada S., Taketo A.;
**Northeotide sequence of the genome at the bacteriophage alpha 3:
interrelationship of the genome structure and the gene products with
those of the phages, phi X174, G4 and phi K.";
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                     Pokaryota: Metaroa; Nematoda; Chromadorea; Khabditida, Ehabditoidea.
Khabditidae; Peloderinae; Caenorhabdilis.
NCBL_TaxID 6249
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1. Biol. Chem. 254.12615-12628(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.1%; Score 69; DB 1; Length 1788; 28.9%; Pred. No. 45;
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SEQUENCE 1288 AA; 2006(3 MW; 8FLADARI9B20A2 CRCCA);
                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1995) to the EMBL/GenBank/DDRT databases
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NGBL_TaxID=10849;
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01-JUL-1994 (Rel. 26, Last Sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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                                                                                                                                                                                                                                                                                      Leimbach D., Waterston R.;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidue, Homo.
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LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (LDL RECEPTOR).
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Post torid Similatity 18.0%; Pred. No. 3.2;
Matches 28; Conservative 11; Mismatches
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MEDLINE-85024898; PubMed-6091915;
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MERCINE 96140036, FubMed-3005267;
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21-JUL-1986 (Rel. 01, Created)
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                                                                                     Meiner V., Landsberger D., Berkman N., Peshef A., Seqal P.,
Softel H.C., van der Westhayzen D.R., Jeenah M.S., Coetsee G.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Common mutations in the low-density-lipoprotein receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                felli N. Garuti P. pedrazzi P., Chisellini M., Simone M. I.
iozzo K., Cattin L., Valenti M., Bolleri M., Bertolini S.,
Stefanutti C., Calandra S.;
'A new missense mitation (Cys297...rbc) of the lew density
'A new missense mitation (Cys297...rbc) of the lew density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lipoprotein receptor in Italian patients with familial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intracellular movement of receptors.";
Proc. Natl. Arad. Sri. B. S. A. R6.4166-4170(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAPIANTS PH SWEDISH LYS 277, THP 423 AND ASK-979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS FH PORT HIS-401 AND THRKH ASP-844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kolvisto U.-M., Vilkari J.S., Kontula K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARLANTS FH LYS-140; SER-338 AND LEU-685.
MEDIJINF-96011600; PubMed=7583548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT FH FRENCH HIS-564.
MEDLINE-96055F24; Pubmed-7550239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDITNF-94222419; Pubmed 8168830;
VARIANT FH PISCATAWAY.
MEPLINE-91328152; Pubmed-1867200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypercholesterolemia (FHTrieste).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MFDLINE-96029270; PubMed-7573037;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.538-540(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutat 6.87-88(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT FH TRIESTE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAFIANT FH ZAMBIA.
                                                                                                                                                                                                                                                                                                                                                                                          VARIANT FH SAFED
                                                                                                                                                seiter B.C., Var
Leitersdorf E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hadjian A.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamanoto A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING PROBABLY OCCURS, GIVING
                                                                                                                                                                                                                                                                                                                                                                                                                   202 FRALSARCTHISSWAPTWAGPROKRIKSDERNCAVATCRPDRF---OCSDONCTHISSROCDRE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 YDGKDMSDRVGGVNVTLABGPN-KFKO---BSGBATTLAKVGNMAPFGPPWSDPPFKBGG 314
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                         8 FACVLFCMVHKAALAD-----DK------TCNPTDFMVTQT1TGLT1GCKGEF--- 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 ------EVNLINNLYCAQSNVKVSCBGLHTTEPIDPHII------RPLSD-----G 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: EXPRESSED IN TISSUES AND CELLS IN WHICH THE MYSGLOGIN GENE IS TRANSCRIPTIONALLY ACTIVE (CARDIAC AND SKELETAL
Ekstroem U., Abrahamson M., Sveger T., Lombardi P., Nilsson-Ehle P.
                  "An efficient screening procedure detecting six novel mutations in
the LDL receptor que in Swedish children with
hypercholosterolemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IOL COLL BIOL 14:4596-4605(1994).
PUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO THE UPSTREAM ENHANCER ERGION (CACK BOX) OF MYOOLOBIN GENE. HAS A ROLE IN MYOGEN!" RIFFEERITATION AND IN REMOTE BLURS FROMESSES OF ACULT
                                                                                                                                                                                             Leren T.P., Solberg K., Rodningen o K., lonstad S., \log \sigma(1) "Two novel point mutations in the EGF precursor homology domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Myoryto nactor factor, a most winged-balla transmights factor under both developmental and neural regulation in striated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculas (Mouse).
Bukaryota, Motaron, Chordata, Cramiata, Vortebrata, Enteleostemi.
Mammalia, Butheria, Pedentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUSCLES THAT OCCUR IN RESPONSE TO PHYSTOLOGICAL STEMULI SUBCREGUEAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                    Ouery Match 9.98; Score 68; DB 1; Length 860;
Best Local Similarity 24.78; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                        13; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2009 (Rol. 39, Last annotation update)
FORRHEAD BOX PROTEIN KI (MYOCYTE NUCLEAR FACTOR) (MNF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hermandez M D , Yang Q , Rochelle J M ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: PHOSPHORYLATED.
SIMIIAPITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              517 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 TNNCLVNNGAPISHATLVAFKYAWDVPPSFSIIS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 TNECLDNNGGCSHVCNDLKIGYECLCPDGFQLVA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RISE TO TWO DIFFERENT TRANSCRIPTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 1 FHA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                         MEDLINE-95362260; PubMed-7635482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94277065; PubMed-8007964;
                                                                                                                                                 VARIANT FII NORVEGIAN ASN-487 DEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
                                                                                                Hum, Genet, 96:147-150(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seldin M.F., Williams R.S.;
"Myoryto nuclear fortar, a n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYOCYTES, BRAIN, KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L26507; AAA37529.1; -
                                                                                                                                                                                                                                                                                                                        38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCB1_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bassel-Duby P ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOXK1 OR MNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myocytes.";
Mol. Cell. F
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P42128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FXK1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 GKGSFWPTDPASEAKIVEQAFPKPPQPGVSCFFTDFGPLSSPRSPASPTHPGLMSPRSSG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- CAFALYTIC ACTIVITY: SERVERENTIONSE 7-PHOSPHATE + D GLYCEPALDEHYDE 3-PHOSPHATE = D-KIBOSE 5-PHOSPHATE + D-XYLULOSE 5-PHOSPHATE.
-i- COFACTOR: THIAMINE PYROPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                  26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    45 GKQEF------EVNLINNLYCAQSNVKVSC------DGLHTTEP1DPH11RP1,SDG 88
                                                                                                                                                                                      DNA-binding, Transcription requiation, Activator. Nuclear protein, Phosphorylation, Alternative splicing, Differentiation. DOMAIN DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria: Firmicutes: Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEATH-ALDC 29342 , M129,
MEDLINE-97105885; PubMed=8948633;
Himmelreich R., Hilbert B., Plaqens H., Pirkl B., Li B. C.,
                                                                                                                                                                                                                                                                                                                                          DB 1; Length 617;
                                                                                                                                                                                                                                                                                                                                                                                  38; Indels
                                                                                                                                                                                                                                                                288 379 FORK-HEAD.
617 AA: 65839 MW; A1083H28C709FC4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 -- TNNCLVNNGAPISH ----- ATLVAFKYAWDVPPS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 LQTPECLSREGSPIPHDPDLGSKLASVPEYRYSQSAPGS 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (Rel. 40, Last annotation update) TRANSKETOLASE (EC 2.2.1.1) (TK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSTTE; PS00801; TRANSKETOLASE_1; FALSE_NED. PROSTTE; PS00802; TRANSKETOLASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 24.2%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to licensetisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mucleis Acids Ecs. 24:4420-4449(1996).
                                                  Pram; PF00498; PHA; 1.
Pram; PF00209; Prof. lead; 1.
PROTIE: PROD053; POPKHEAD.
PROSITE: PS00557; POPK_HEAD.]; 1.
PROSITE: PS00557; POPK_HEAD.]; 1.
PROSITE: PS500549; POPK_HEAD. 2: 1.
PROSITE: PS50006; POPK_HEAD. 3: 1.
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                                                                                                                                                                                                                                                                                                                                                                                  24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
MGD; MGI:1347488; FOXK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma pneumoniae.
                InterPro; 1PR000253;
InterPro; 1PR001766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P23254; 1TKA.
InterPro; IPR000360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                              27
107
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                                      InterPro;
                                                                                                                                                                                                                                                                    UNA_BIND
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Transferase, Thiamine pyrophosphate.

24122 MW; CP2958BDB2R755BC CRC64;

: The AM;

SECUPION

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                                                                                                                        5.IC
                                                                                                     52 NLINNLYCAQSNVKVSC · · · · DGLHTTEPIDPHI · · · · · · IRPLSDGT - · NNCLVNNG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SURCELLULAP LOCATION- INTEGRAL MEMPRAME PROTEIN.
-1- SIMILARITY: BELONGS TO PAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                         Eukarycia, Metarra, Chordita, Croninta, Vertekinta, Futylyssiumi,
Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Organization and evolution of olfactory receptor genes on human
                                                                          G*-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99005533; PubMed-9787077;
Buettner J A , Glusman G , Ren-Arie N., Eamos F., Lancet D.,
                                                                                                                                                                                                                                                                                                 01-0cT-2000 (Rel 40, Created)
01-0cT-2000 (Rel 40, Last sequence update)
01-0cT-2000 (Rel, 40, Last annotation update)
0LFACTORY RECEPTOR 5D4 (CLEACTORY PETERTOR 11-8C) (CP11-9C)
                                          Score 67; 78-1, Longth (18.)
Pred, No. 17,
                                                                        23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PSAG277: 7. PHATEIN_PEREP_F1_1; 1.
PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELEULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLUIAR (FCTENTIAL)
648 AA; 72378 MW; EFE8247D7F9837/19 1P/164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POPENTIAL)
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                                                                        8. Mismatelass
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BY SIMILARITY
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                                                                                                                        357 NSNSNLYCLNADVARSCNIKLGDDNLHT
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                                                     Similarity 31.0%,
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                                                                        22; Ornservative
                                                                                                                                                                                                                                                                        STANDARD:
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Pfam; PF00001; 7+m_1: 1
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                                                                                                                                                                 98 APISHATLVAF 108
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09UP62;
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This SWISS FROT coulty is copyright. It is produced through a collaboration between the SWISS Institute of Bloinformatics and the EMBL outstation the Furgipean Rioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities required a liberal and prement (See Althoughway Isbasib elydmonunce) or send an email to liberasedish-sib.ch.
                                                                                                                                                                                            94 YFLLTLSFCRTNFINNFVCEHAAIVAVSCS------DPYMSGKVILVSATFN---- 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Allergers of wild house dust mites, environmental Der p 1 and Der p sequence polymorphisms.";
Submitted (JHN 2000) to the SWISS-PPOT data bank.
                                          Galus
                                                                            7 FFACVI POWVHK---AALADDK---FONPTDFWV--TQTTTFLTLTLCAKQBFBV----- 51
                                                                                                        52 ------LSDGTNNLYCAQSN-VKVSCDGLHTTEPIDPHIIRP--LSDGTNNCLVNNG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Antigonic and structural analysis of group 11 allergens (Der f II and Der p II) from house dust mites (Dermatophagoides spp)."; J. Allergy Clin Immunol 83:1055-1067(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachaida, Acari;
Acaritormes: Sarcoptiformes; Astigmata; Analgoidea; Pyroglyphidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Tertiary structure of the major house dust mite allergen Der \mathfrak p 2. sequential and structural homologies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Simpson P <sup>T</sup> , Turnor M <sup>T</sup> , Stowart G A ,
                                          40, Indels 45,
    198 1. Length 216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arch. Allergy Appl. Immunol. 91:118-123(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                            01 OCT 2000 (Rel. 40, Last annotation update)
MILE ALLENGEN LEE F 2 DECUMBER (DER P II) (DPX).
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                                                                                                                                                                                                                                                                                                                                                                      146 AA.
  Scare FA 5, 10
Pred. No. 5.4;
                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90256301; PubMed=2341191;
Chia K.Y., Doyle C.P., Simpson P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE 892/8484; PubMed 2/32406;
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01-FEB-1996 (Rel 33, Last sequ
    5.78,
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                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                      Lucal Similarity
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"Analysis of tardwar mutiple genes encowing 39 kDs membrane proteins
in Pasteurella harmolytica Al.";
Gene 129:107 111(1993).
                                                                                                                                                                                                                                49 FEVNIJINNLYCAQSNVKVSCIX3LHTTEF-IDPHIIRPLSBGTNNCLVNNGAPISHATLVA 107
                                                                                                                                                                                                                                              58 FEAN--ONTKTAKIEIKASIDGLEVDVPGIDPNACHYMK-------CPLVKGOOYD-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cooney B.J. Lo R.Y.C.,
"Three cantiguous lipoprotein genes in Fasteare'la haemolytiva Al
Which are homologous to a lipoprotein gene in Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPID
                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, gamma subdivision, Pasteurellaceae,
                                                                                                                                                                                                     9.6%; Score 66; DB 1; Length 146;
                                                                                                                                                                               59182FA7FD2653AF CRC64;
                            MITE ALLERGEN DER P 2.
                                                                                                                                                                                                                                                                                                                              01-MOV-1995 (Pel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
OUTER MEMBRANE LIPOPROTEIN 2 PRECURSOR (PLP2),
             Allergen; Signal; 3D-structure; Polymorphism.
                                                                                                                                                                                                                                                                                                           276 AA.
                                                                                                                                                                                                           Pred. No. 3.9;
6: Mismatches
                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SEKOTYPE AL;
MEDLINE:93328110; Pubmed=8335249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE 94011478; PubMed-8406866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immun. 61:4682-4688(1993)
                                                                           エウイストニロシット>
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01-NOV-1995 (Rel. 32, Created)
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EMBL; AF276239; AAF86462.1;
PDB; 1A9V; 14-OCT-98.
                                                                                                                                                                                                           29.48;
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                           Pasteurella haemolytica.
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136
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                                                                                                                                                                                146 AA;
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                                                                                                                                                                                                                                                          108 FKYAWDVP 115
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                                                                                                                                                                                                                                                                                                                                                                         Mannheimia.
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                     SIGNAL
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                                                                                                                                                                                            extitios implies a librase agreement (See http://www.isb.ch/incomercial or send an email to license@isb.ch).
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15-JUL-1998 (Rel. 86, Last annotation update)
SERINE-TYPE CARBOXYPEFITIDASE F PRECURSOR (EC 3.4.16.-) (PROTEINASE F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 ATENDIIENPKNIKIVQADTSLLTRMLDDDVELAVINNTYAGQAGLSPDKEGTIVESKDSP 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins and paptide synthesis.";
AFFL Exylenc. Mirchiol. 58:2114-2152(1992).
-!- FUNCTION. REMOVES ANY ACID FROM THE C TERMINDS OF A LONG
PEPTIDE. DIGESTS PREFERENTIALY PEPTIDES CONTAINING A POSITIVELY
CHARGED RESIDUE IN P1' POSITION, AS WELL AS ARGININE, LYSINE OR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Fungi, Ascomycota, Peninemycotina, Entotlomycotes,
Functiales, Trichoromarous, mitosporie Trichoromaroae, Asporqillus,
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"Furification and charactorization of two sorries corboxypoptidases
from Aspergillus niger and their use in C-terminal sequencing of
                       SIMILARITY: BELONGS TO THE NIPA FAMILY OF LIPOPROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-ACYL DIGLYCERIDE (PROBABLE).
FNG -> LTVH (IN PEF 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OUTER MEMBRANE LIPOPPOTEIN 2.
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Sukwitted (OCT 1997) 1. The FMHL/OPERPOR/ISHR: databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer membrane; Lipoprotein; Signal; Multigene family.
SIGNAL
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MEDLINE-92344370; PubMed=1637154;
                                                                                                                                                                                                                                                                                                                                                                                                                 PPOSITE; PSOCO13; PROKAP_LIPOPPOTFIN: 1
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MEDLINE-95119895; PubMed 7828908;
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Matches 16; Conservative
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270
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ANCHOR (PROBABLE)
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276 AA:
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P52718;
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RESULT 14
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       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions in the modified and this statement is not removed. Swape by and to commercial entities requires a license agreement (See http://www.ist.i.el.commercial
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                                                        INDUCTION: IN THE POLLOWING GROWTH CONDITIONS: ACTUAL PH, ABSENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 PSVESVEVGGGGGGPEGEGFSANPTF-HVLFQVIEGTNEVLIGNGDYDMV ULTNGTLLST 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 Gaps
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                                                                   OF NITROGEN OR CAPRON SOUPPE
SIMILANITY, BELORGS TO PPPTITASE FAMILY 310, ALSO FRAGILAS THE
ENCYME IS SHRIAHLH ABOVE PH B. CATALYDE ALAC FEFTIUL CTHTHESIA
CATALYTIC ACTIVITY: RELEASE OF A C-FERMINAL AMIN' AND WITH A
BROAD SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                           SERINE-TYPE CARBOXYPEPTIDASE F.
                                                                                                                                                                                                                                                                               PROSITE, PSOOIAL, CARBOXYPEPT_SER_SEP, 1.
PROSITE: PSOO560: CARBOXYPEPT_SER_HIS; 1.
Hydrolase: Garboxypertidase; Glycoprotein, Hydrolase; Garboxypertidase; Glycoprotein, Hydrolase; Slqual.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 6%; Score 66; DR 1; Length 531,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KODPOPA9P847R550 CRC64:
                                   ENSYME REGULATION, INHIBITED BY LEFP, AND HG (CL) 2.
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-> F (IN REF. 3).
-> Y (IN REF. 3).
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01-OCT-2000 (Rel. 40, Last annotation update)
HISTIDINE DECARBOXYLASE (EC 4.1.1.22) (HDC).
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                                                                                        SERINE CARROXYPFPTIDASE FAMILY
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84
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                                                                                                                                                                                                      EMBL; X79541; CAA56075.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          443 QNMTWNGKLGFDTAPSTPI 461
                                                                                                                                                                                                                EMBL; L33408; AAB57723.1; -. HSSP; P10619; 1IVY.
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                                              SUBUNIT: MONOMER.
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between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by most profit institutions as long as its content. Is no way modified and this statement is not removed. Usage by and for commercial entities requires a increme and the Commercial or send an email to licensectables (See Mith Naww ishesh ch/announce).
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Lydac. Decarboxylase, Catecholamine biosynthesis: Fyridoxal phosphate.
BINDING 305 905 PRIDOXAL PHOSPHATE (POTENTIAL).
SECURING 148 S -> Q (IN REF. 1).
SECURING 152 AA, 74:40 MW. PP611CRARG60469 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE 92119328; PubMed-1768863; ...in. w. A. i. F. M. Mostif. w. M. Joseph D.K.; and e. i. M. Mostif. w. M. Joseph D.K.; and the converse of the converse from an erythroleukemia cell line and mapping of the gene locus to chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
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Victoria E., Buribo S., Shawara Y., Taner V., Machania K.,
Watanabe P., Satoh K., Yoshizawa M., Shibahara S., Takishima T.,
Watanabe P., Satoh K., Hoshizawa M., Shibahara S., Takishima T.,
Watanabe P., Naciecilla Sequence of the cDNA encoding L histidine decarboxylase
derived from human busephilic lenkemia cell line, KU-812-P.";
Nucleic Acids Res, 18:5891-5891(1990).
Homo sapiens (Human).
Edkaryota, Metaica; Chordata; Chamiata; Vertebrata; Enteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yatsanami K., Ohtan H., Isuchikawa M., Hiquchi I., Ishibashi K.,
Shida A., Shima Y., Nakagawa S., Yamauchi K., Yamamoto M.,
Hayashi N., Watanabe T., Ichikawa A.;
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                                                                                                                                   Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-:- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Survey N. Watanabe T., Tehikawa A.; "Structure of the L-histidine decarboxylase gene."; "Structure of the L-histidine decarboxylase gene."; " Biol. Them. 269:1554-1559(1994).
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MIM; 142704; -.
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Matches 31; Conserv
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                                                                                                                                                                                                                                                                Kalinski A., Rowley D.L., Loer D.S., Foley C., Buta G., Herman E.M.; "Binding-protein expression is subject to temporal, developmental and stress induced regulation in terminally differentiated soybean
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                                                                                                                                                                                                                                                                                                                             Planta 195:611-621(1995).
                        01-0cT-1996 [kel. 44, Created)
01-0cT-1996 [kel. 44, Last sequence update)
01 NOV-1992 [kel. 45, Last concotation update)
01 NOV-1992 [kel. 45, Last concotation update)
GLOCAN ENDO-1, **BEIA GLOCAN DARFER [FE 4.2, 1.49] (() + 3) BEIA GLOCAN ENDO-4, **BEIA GLOCAN DARFER [KETA 1, ***ENISAGISTAN ASE)
                                                                                                                                       Eukaryota: Viridiplantae; Embryophyta; Tracheophyta: Spermatophyta;
                                                                                                                                                      Magnoliophyta; eudicotyledons; core endicots; Rosidae; enrosids I;
Fabalos; Fabareae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (Ref. 40) tast sequence update)
61-0CT-2000 (Ref. 40) tast annotation update)
CYPOHLASMIC PROTEIN NCK2 (RCK ALAFICE FRO TEIN 2) (FEZ/SH3 ALAHIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO FAMILY 17 OF GLYCOSYL HYDROLASES.
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26.4%; Pred. No. 9.5;
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255 AA; 27671 MW; 12A23BFFFF1B3611C CRC64;
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PROSITE: PS00587; GLYCOSYE_HYDROL_E17; 1.
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Now TER
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                                                                                                                                                                                                                                  STRAIN CV. CENTURY 84; IISSUE Leaf;
MEDLINE:95218610; PubMed:7766051;
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STANDARDS
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                                                                                                                        Glycine max (Soybean)
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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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0436393
WI 3B SOYBN
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no testrictions on its more by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreedant (over http://www.isb.sib.chgannann.co. or send an email to licensegisb:sib.ch).
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Cleen M., She H., Davis E.M., Spicer C.M., Kim L., Ren K., LeHeau M.M.
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                                                                             Li W.; "Lidentification of New Lawilly genes, chromosomal localization.
                                                                                                                                      expression, and standing specificity.";
i. biol. Them. 273-2517-45178(1994).
·!· FUNCTION: ACAPITE FEATELW WHITH ASSOCIATES WITH IYEQUINE
PHOSPHORYLAIED GROWTH FACTOR RECEPTORS OR THEIR CELLAILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Indels
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29.5%; Pred. No. 15;
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                                                                                                                                                                                                                                                                                   !- SUBCELLULAR LOCATION: CYTOPLASMIC.
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Best Local Similarity 29.5%
Matches 18; Conservative
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InterPro; IPR001452; -.
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Piam; PF00018; SH3; 4.
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SECUTENCE FROM N.A.
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196
286
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OM profein - protein search, using sw model

July 18, 2001, 17:27:28 ; sourch time dill seconds (Without alignments) 802 609 Milling well update;/ Run on:

Title: Perfect score:

Sequence

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

4.25026 Total number of hits satisfying chosen parameters:

425026 seqs, 132305027 residues

Searched:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_16:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_tungi:*
5: sp_tungi:* sp_mhc:* sp_organelle:* sp_phage:* sp_mamma]:*

sp_unclassified.*
sp_vertebrate:*
sp_virus:* sp_plant:*
sp_rodent:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Persolt.	Score	& Guely Match	* Çuel; Match Length DB	UR	1D	Description
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្ព	75	10.9	326	m	042851	012861 schizosacch
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14	73	10.7	2349	~	P94750	P94750 escherichia
<u>\$</u>	73	10.7	2383	ា	P76347	P76347 escherichia
16	72.5	10.6	366	P.,	013522	013522 sancharomyc
17	7.2	10.5	1261	10	Q9LYB5	Q91yb5 arabidopsis
18	7.1	10.4	535	~	09X4D1	Quaddlactinumycos
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10 09F1W7 14 ceptib8 1 026626	14 Q82008 5 Q23488 14 Q9DKT9 2 O56952	to <u>c04617</u> 10 09MIS3 10 <u>0</u> 9LIX68	4 090H51 10 024080 10 023982	7 945429 11 0921R2 2 068223	5 U96259 5 QDD974 5 Q44924 5 Q9W213	14 090004 4 095220 2 00%93	4 plu465 2 054292 1 09VIEI
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# ALIGNMENTS

RESULT 1 0928J7 15 Q928J7 FRELIMINAKY, PKT; 128 AA.	AC (9229J7; pm 01:wav:1609 /TrpMB1rol 10 Created)	01-MAY-1999 (TrEMBLrel. 10,		D8 1,051.			ы: Maquoliophyta; Eiliopsida: Liliales; Liliaceae; Lilium.					Xu H., Swoboda I., Bhalla P.L., Singh M.B.;	RT "Male dametic cell-specific gene expression in flowering plants.";		DR EMBL; AF 10779; AAD19962.1; -	SQ SECTIONSE 128 AA, 13851 MW, FERGAFICIONELBEITA ORCEAU		100 00 Secto 685, 18 10, Longth 128; Harity 100.00; Prod. No. 1e-68;	atire	Qy I MEAVAVEFACVLFCMVHKAALALDINKTCNPTDFMVTQTTFGLTFGGROPFFVNI INNLYCA 60			Oy 61 SSAWKVSCUGEHITEFTIJEHITKELSJÖTINIGEVNIGAFISBATIVAFKYAMDVPPSESI 120	Db 61 OSNVKVSCDGLIJTTEPTDFHLIKPLSDGTNNCLVNNGAPTSHATLVAFKYAWDVPPSFS1 120		97 1.21 ISSUINGS 128	THE TOTAL TOTAL
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Submitted (MAR-2000) to the EMBL/Schrädak/DDBL databases.
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                                                                                                                                                                                    Eukaryola: Viridiplantae: Embryophyta: Tracheoplyta: Spermatophyta: Magnoliophyta: endicotyledons, core endicots: Rosidae; eurosids II; Brassicales; Eussicaceae; Arabidopsis.
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Enkaryota: Vildipiantae: Emblyophyta: Fracheophyta: Spermatophyta:
Mannollophyta: eudie tylebus: core evaliets; Fesidae: cur.sils It:
Brassicates; Hassicaceae, Atabidopsis.
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Moone Hita Marger K. Schooller C
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Submitted (MAK-2000) to the EMEL/Condere/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1998) to the EMBL/ConHabk/DDW+ databases.
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                                     01-00N-1998 (TrEMBLIC). 06, Created)
01-00N-1998 (TrEMBLIC). 06, Last sequence update)
01-00T-2000 (TrEMBLIC) 15, Tast amoiation update)
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01-JUN-1998 (TrEMBLIC), 06, Last sequence update)
01-OCT-2000 (TrEMBLIC), 15, Last annotation update)
124 AA
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                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
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F10N7.100 OF A14632696.
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PRELIMINARY;
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Lenne Ser No. 2. Mayor K.F.X.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          35 VIOSKIGNMVENKPEWEVKVLNSSPOYFTHTTL,SCVRFKSVTP1DSKV L,SKSODTCL, 91
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Magnoliophyta, codicolyledons, core endicols; Rosidae; eurosids 11;
Brassicales, Brassicaceae; Arabidopsis.
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31.6%: Pred, No. 7.2e-07;
.ive 17; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.1%; Score 124; BB 10; Length 264; 31.7%; Pred. No. 6.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bevan M., Koetter P., Hempel S., Entian K.-D., Hoheisel J.,
Mewes H.W., Mayer K.F.X., Schueller C.,
Submitted (JAN 1998) to the EMBG/Grenbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
EU Arabidopsis sequencinq project:
Submitted (MAR-2000) to the EMHL/GenBank/DDBJ databases.
EMBL: ALD2168; CAB79928.1; ...
EMBL: ALL61580: CAB79928.1; ...
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Submitted (MAR-2000) to the EMRL/GenBank/1993 databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL chemine from the desired
                                                                                                                                             Hypothetical protein.
SEQUENCE 124 AA; 13797 MW: 974AEEC740F24F80 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09, Last sequence update)
16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 VNNGAPISHATI,VAFKYAWDVFPSFSIISSDINGS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 LONGESTHEFF - LISTRY VWOLLSPELIK VVOOTY LACK 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TIEMBLIEL, 06, Created)
01-JAN-1999 (TERMBLIEL, 06, Last sequence
01 MAK 2001 (TEMBLIEL, 16, Last annotative
BYPOTHEFICAL 40.0 KDA PROTEIN (PRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
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submitted (MAR 2000) to the PMR(20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mendel; 27485; Arath;3257;27485.
InterPro; IPR002659; -.
                                                                                                                 Mendel; 28142; Arath;3257;28142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: AL021636; CAA16578.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL161580; CAB79929.1;
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                                                                                                                                                                                                                                                                                             Best Local Similarity 31.69
Matches 20, 7 macratime
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NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       049381;
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1057 ASVVQFTCVQMSKPLKFLLWSSLALLLLQIGSGAIGPGKSSFPA---VFGTGVKWREGKK 1113
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Liu S.X., Sakano H., Yu G., Toriumi M., Lonz C., Loc Jum., Li J.,
Liu S.X., Sakano H., Yu G., Toriumi M., Lonz C., Loc Jum., Li J.,
Luu A., Gonzalez A. Liu K., Vaysborg M., Chin C., Hwert B., Chol C.,
Chiou J., Pham P., Roo T., Altafi H., Bronks S., Bachler E., Chan Q.,
Conn L., Conway A.B., Hanson N., Johnson-Hopson C., Khan S.,
Lam B., Nguyen M., Palm C., Shinn P., Tambunga G., Davis R.W.,
Eckerspiel N.A., Theologis A.;
Arabidopsis thaliana chromosome i BAC L20M3 sequence.";
Submitted (FEB-2010) Lo. Lhe EMBL/GenBank/HDBJ databases.
EMHL: AC099999: AAF29390.1;
Interpro; IPP000438.
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Tomink S., Hefsann E., Nix K., Pastasson M., Stoffol W.;
"Cloued mammalian neutral sphingemyelinase, functions in sphingelipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 QEFEVNLINNL PCAQSNVKVSCDGLHTTEPIDPHILEPLSDGINNCLVNNGAFISHAIL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23, Julia
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                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermalophyta,
Mannellophyta, endisetyledoms, cotecendients, besidae, veresids itt
Brassicales, Brassicaceae, Arabidopsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metaroa, Chordata, Graniata, Vortebrata, Entoleogtemi,
Mammalia, Eutheria, Rodentia, Selurognathi, Muridae, Mulinae, Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.0%; Score 116.5; DB 10; Length 1193; 27.8%; Pred. No. 0.00026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51, indels
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01-MAR-2001 (TrEMPLrel. 16, Last annotation update)
SPHINGOMYELIN PHOSPHORIESTEPAGE 2 (EC 3.1.4.12) (NEGTEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMAKT; SM00249; PHD; 1.
SEQUENCE 1193 AA: 125416 MW; 4P2B3D5776A30DP5 GENT4;
                                                                                              01-OCF-2000 (TrEMBLrel. 15, Greated)
01-OCF-2000 (TrEMBLrel. 15, Last sequence update)
01-MAE-2001 (TrEMBLrel 16, Last apportation update)
120M5.10 PROTEIN
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                                    PPT: 1193 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE, PS00190; CYTOCHROME_C; UNENDWN_1.
                                                                                                                                                                                                                                                                                  Atabidopsis thaliana (Mouse-ear cress).
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                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ptam; PF00855; PWWP; 1.
Ptam; PF00856; SFI; 1.
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InterPro: IPRU01965; -.
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Matches 35; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702
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                                                                                                                                                                                                                                         F20M3.10.
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                                                                 09MA4 3:
                                Q9MA4 +
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Q9MA43
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                                                                 A PART OF THE PART
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Politorak A., Smirnova I., He X., Liu M.-Y., Van Huffel C., Firdwoll D., Alejos E., Silva M., Du X., Thompson P., Chan B.K.L., Lodesma J., Roce H., Clifton S., Vogel S.N., Bettler H., Schreite and physical mapping of the Ips locus: identification of the foll-4 receptor as a candidate gene in the critical region.", Flood Colls Mol. Dis. 24:340-355(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 BGCTMVP6 NOYVSQQDFGPPSO-----FP DYVLYRAVSFFHVOOF HERT DS70PBSD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.3;
7; Mismatches 40; Indels 19; Caps
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                                                                                                     SUBCELLUIAP L'OATION: INTEGRAL MEMAPANE PROTEIN.
TISSUE SPECIFICITY: ALTHOUGH WIDELY EXPRESSED IN ALL TISSUES
EXAMINED, EXCEPT THE SPLEEN, HIGH ENZYMATIC ACTIVITY OCCURS ONLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 EDKTCHPERPMYTQTITGLIFGRKQEFEVNLINNLYCAQSNVKVSGBGLHTTEPIDPHFF 82
                                                                                                                                                                                                                                                                                                                                                                               MAGNESIUM (BY SIMILARITY).
IMPORTANT FOR SUBSTPATE PECOGNITION (BY
                   -i-- FUNCTION: CONVERTS SPHINGOMYELIN TO CERAMIDE.
-i-- CATALYTIC ACTIVITY: SPHINGOMYELIN + H(2)O = N-ACYLSPHINGOSINE +
CHOLINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryeta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciuroquathi, Muridae, Murinae, Mus.
                                                                                                                                                                                   1- MISCELLANDEGUS: THIS PROTEIN HAS AN OPTIMUM PHOF 6.5-7.5.
MISCELLANDEGS: HEELE ARE TWO INTER: OF SPHINGOMIELLINASES. ASM (ACLD), AND NSM (NEUTRAL).
SIMILARITY: TO OTHER SPHINGOMYELLINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.5%; Score 78.5; DB 11; Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL BASE (BY SIMILARITY).
5812FC630A69C356 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10, Last sequence update)
16, Last annotation update)
Natl. Acad. Sci. U.S.A. 95:3638-3643(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 RELSECTIVING APPROAPRY AND VPP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             835 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                                                                                                                                                                                   Hydrolase; Transmembrane; Magnesium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C3H/HEJ;
MEDLINE-99069627; PubMed 9851930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47466 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stience 282:2085 2098(1998).
EMBL, AF095*5: AAC99411.1;
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Matches 28: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOLL-LIKE RECEPTOR 4 MUTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY,
                                                                                    COFACTOR: MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01 MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                               1278330; Smpd2
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                                                                                                                                                                                                                                                                                                                                         346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCB1_Tax1D=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99051437;
                                                                                                                                                                     IN THE HRAIN.
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                                                                                                                                                                                                                                                                                               MODE MOT:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHOUENCE
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                                                                                                                                                                                                                                                                                                                                         FRANSMEM
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                                                                                                                                                                                                                                                                           EMBI.;
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835 AA; 95518 MW; 9083859F9A220017 CRC64;

SEQUENCE

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258 ILGEFKDFKNLEIFFPSIMEGLÖNVILDEFKLIYINDFSDDIVKFHCLAN·····VSAMSI. 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 LALDMALNPIDFTQDQAFQGIKL - - HELTLEGNF - NSSNIMKTCLQNLAGLHVHRL 25/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 LACHERTONPTDEMVIOTITGLT (GGROEFEVILINNLY/AGSNVRVSC----EGILH---- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Motanda, Chordata, Craniata, Vertebrata, Eur. Foestomi.)
Mammalia: Eutheria: Rodentia, Sciuroquathi, Muridae, Murinae: Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouroshi S.T., Lariviere L., Leveque G., Clermont S., Moore K.J.,
Gros P., Malo D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Endotoxin Tolerant Mice Have Mutations in Toll-Like Receptor 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                               497
                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Material 11.3%; Score 77.5; DR 11; Lenath 845; Best Local Similarity 24.5%; Prod. No. 3.7; Matches 44; Indels 49; Matches 44; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1999) to the FMRL/GenRank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                 SEQUENCE 845 AA: 95558 MW: 909535911A3A0017 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLiel, 13, Created)
01-MAY-2000 (TrEMBLiel, 13, Last sequence applate)
01-MAR-2001 (TrEMBLie) 16, Tast amodation applate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Poltorak A., Smirnova I., Chan E.K.L., Beutler B.; "Genetic variation at the TLR4 locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00019; LEUKICHRPT.
PROSTTE; PS00159; ALDOLASE_KDPG_KHG_1; UNKNOWN_1.
                                                                                                                                     PTAMES PRODUCES THE LEGISTER P. PRINTS: PRODUCES PRODUCES PRODUCES PROGUES PROGUES ALFOLASPER PROGUES: THE PROPUSE PROCESS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 AGVSTRYLEDVPRHFRWUSISITE: 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIJINE-99145502; FibMed:9989976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exp. Med. 189:615-625(1999).
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EMBL, AF110133, AAD29272.1; -..
MGD, MGT-96 R24, T114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR000887; ...
InterPro: IPR00161]; ...
PTam: PE30560; LRP: 7.
Ptam: PF31453; LRROT: 1.
Ptam: PF01582; TLE: 1.
                                                                              Pfam; PF00550; LRR; 7.
Pfam; PF01463; LRRCF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                            SMART; SMOJ255; TIR; 1.
Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00255; TIR; I. Receptor.
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01-MAR-2001 (TrEMBLIF)
EnterPro: IPR:100484; -
                                                                                                                                                                                                                                                                                         712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                      InterPro; IPRO01611;
                              InterPro; IPR040887;
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                                                                                                                                                                                                                                                                                         71.2
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                                                                                                                                                                                                                                                                                         VARIANT
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                                                                                                                                                                                    NNCLVNNGAPTSHATE, 105
                                                                                                                                                                                                                                                                                                                                                      258 ILGEPKDEKNIETFEPSIMFOLOVITDEFKLITYTNDESDOIVKFHÜLAN -- - VSAMSL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sales
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 LHTTE--PIDPH11RPLSIX31NNCLVNKGAP1SHAFLVAFKYAWD-VPPSFS11SSD1-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22] HRISEGPKYPGTHNPLDD INFILE - HDTSGTEKYYRTRIVE EFFN 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thallana (Mouse-ear cress).
Bukaryota: Vilidiplantae: Embryophytu; Tracheophyta; Spermatophyta:
Maqnoliophyta, eadlectyledons, core endicots, kosidae; eurosids II;
Brassicales: Brassicaeae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sate S., Nakammra Y., Kaneko T., Kate I., Asamizu E., Tabâta S., Sutmitted (JAN 1999) to the PMH AsenBank/NDBJ databases.
                                                                                                                                               21 TAPDETONFUDEMVIQTUTGILIGSKÆFTEVNI INNI YTAGSNVEVET - - - (*) H---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
                                                                       7.67
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11.4%; Score 77.5; DB-11; Length 845; 26.9%; Pred. No. 3.7;
                                                                   43; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Indels
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01-ADG-1998 (TEMBLEGL. 07, Last sequence update)
01-MAY-2000 (TFEMBLEGL. 14, Last annotation update)
SPHINGOMYELLINASE) (NSMASE).
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EMBL; AB022215; HAB17274.1; -.
SEQUENCE 333 AA; 37450 MW; BGC21350DBDB30B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                   14; Mismatches
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                                                                                                                                                                                                                                                                                      73 -----TTEPIDPHIIRPLSBGT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                  146 --VAFKYAMINVPESFS11S-SPINC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 AGVSTKYLEDVPKHFKWQSLSTIRG 338
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                                                                   39; Conservative
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Best Local Similarity
                                     Best Local Similarity
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Query Match
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                                                                                                                                                                                      Tomink S., Bofmann K., Nix M., Zumbansen M., Stoffel W.; "Poned mammalian beutral sphingomyolinase; functions in sphingolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.9 FEVNI INNIMORQSNVKVSCDSLHTTEFTDFHTTFFTLSPGTNNGLVQBDACT 3HACT VAF 110.9
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IMPORTANT FOR SIRSTRALE RECOGNITION (RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bassetti M , Adetem A.;
"The Toll-like receptor 2 is recruited to macrophage phagesomes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metassa, Cherdata, Graniata, Vertibiata, Euloleosilmi:
Mammalia, Eutheria, Kodeniia, Sciurognathi; Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20014145, FubMad 10548109,
Underhill D.M., Otinsky A., Hajjar A.M., Stevens A., Wilson C.R.,
                 Homo sapiens (Human).
Eukaryotu, Mitazou, Shordatu, Chamiatu, Vertebratu, Eutelemstumi.
Mammalia, Eutheria, Primatos, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                               N ATTENDED TO THE
                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANDOUS: 141S PROTEIN HAS AN OFFIRMON RECUE 5.5 7.5. MISCELTANDOUS: THERE APE TWO TYPPS OF SPHINGOMYELINASES: ASM
                                                                                                                                         SEGGENTE FROM N.A., PHAPATIFFIZATION, AND TISSUE SPECTED MEDLINE-98188255; Pubmed-9520418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL BAŠE (BY SIMILARITY).
05752A923E353171 CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.1%; Score 76; DB 4; Length 423; 32.4%; Fred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Indels
                                                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: MAGNESTIM
-!- SURCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13, Created)
13, Tast sequence update)
16, Last annotation update)
                                                                                                                                                                                                                                                        G Na+1 Arad, Sri H S A GETTRAR-A643(1998)
FUNCTION: CONVEKTS SPHINGOMYBLIN TO CERAMIDE
FATALYTIC ACTIVITY: SPHINGOMYBLIN + H(2)? A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R35 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ACID), AND NSM (NEUTRAL).
--- SIMILAKITY: TO OTHER SPHINGOMYELINASES.
EMBL; AL222E01; CAA10995.1; ...
MIM: 603498; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Transmembrane, Magneslum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       discriminates between pathogens.";
Nature 401:811-815(1999).
EMBL; AF185285; AAF04278 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47592 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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InterPro; IPR001611; -.
Pfam; PF00560; LRR; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (Tremplie)
                                                                                                                                                                                                                                                                                                                                        CHOLINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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423 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                          NCBI_TaxID=9606:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354
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SEQUEN'E
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                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                              21 IANDETONITIEMVIOTITICITICAEQEFEVALINALVOAQSAVEVSO --- DGLH
                                                                                                                                                                                               Ouery Match 11 09; Sooro 75 %; DR 11; Jonqth 835; Best Local Similarity 26.9%; Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.9%; Score 75; DB 3; Length 922; 30.4%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.00 Jan
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Stelton J., Churcher C.M.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parrell R G , Rajandream M A., Wood V.;
Submitted (FER 1998) to the FMRL/SecnEack/TORI databases.
-- SIMIIARITY: TO HELICASE C-TERMINAL DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   922 AA; 164593 MW; 90268P6PD2200ASA 0P064;
                                                                                                                                   HAS AA; WEGHT MW; URANAMIAAAFBESE IPPISA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Fungi, Asbompbota, Schizbsaccharomycetes;
Schibbsaccharomycctales: Schizbsaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 OILSEMSKRVOATAPIS--SLEHFKQLSDISPSFTSSANSIN 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12,
                Pfam; PF01582; TIR; i.
FEINTS: PF00619, FEUFICHRPT.
PF0811E: PS00159; ALTOLASE_KPP0_KHG_L; UNKNOWN_L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               922 AA.
                                                                                                                                                                                                                                                   14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            TEPEDARITHACIATI
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Interpre; IPRODO330; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91-JUN-1998 (TrEMBLICE). 06,
01-JUN-1998 (TrEMBLICE). 06,
01-MAR-2001 (TEMBLICE). 16,
PUTATIVE HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMAFT, SMOO490; HELLIC; 1.
AIP binding; Hellcase.
                                                                                                                                                                                                                                                   Ornservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00176; SNF2_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
Pfam; PF01463; LRRCT; 1.
                                                                                   SMAPT; SMOO255; TIP: 1
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                                                                                                                                 SECTION
                                                                                                                Receptor.
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136 DKLYCAHFNSTHITTYYTSQPLLLEPHVYYEETFFEKGKNDQTN:COGMYTSLKSVHVHTH 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VAVPP-----ACVLIGMVHKAALAFORTONPTHYNAVT2TTFGLITGGELHTUNLINN 56
                                                                                                                                                                                                                                                                                                                                 Oliver K., Bowman S., Harris D., Lawsen D., Quail M., Burrell B.;
Submitted (PEB-1999) to the EMBL/GenBank/DMFC databases.
EMBL: AL034559; CAB39649.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae;
                                                                                                                                                                                                                              Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 10.8%; Score 74; 106.5; Length 1086; Local Similarity 22.5%; Pred. No. 12; Local Similarity 23.5%; Pred. No. 12; Conservative 13; Mismatches 39; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01186; EGF_2: UNKNOWN_2.
SEQUENCE TORK AA: 125891 MW; HET-1600AH5469194 CP064;
                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TERMILLE), 03, Created)
01-MAY-1997 (TERMILLE), 03, Last sequence update)
01-MAR-2001 (TERMILLE), 16, Last annotation update)
                                            1086 AA
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                                                                                                                                                                                                      Plasmodium talciparum (isolate 3D7).
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                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 EPIDPH -- - LIRPLSDOTING 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. 4:379-392(1996).
EMBL: D90836; HAA15799.1; -.
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                                            PRELIMINARY;
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InterPro; IPR00353;
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: 1PR000561;
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Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                                                                                   NCBI_TaxID = 36329;
                                                                                                                                                         PFC1045C PROFEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCPI_FaxID:562:
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                                                                                                                                                                                 PFC1045C.
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RESULT 13
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                                                                                                                                                                 1545 IVTASMIGGRSEGLVVNFTADTLIFAQVNLAVIEDNFTANNVGMTRLQATVITKONDHFLAN 1604
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Report R. Reseauch
M. Makino K.,
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                                                                                                                              47 TITGLTIGGKQE-FEVNLINNLYCAQSNVKVSCDGLHITEPIDPHIIRPLSBGINNCLVN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nikamura Y...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Fremero F., Finda I., Fevera K., Estano A., Itohi I., Karaji K., Kashimoto F., Kim S., Kimara S., Kimarada M., Kitokawa M., Makima Makima S., Kimarada S., Miki T., Mirzerdii K., Weri H., Merepera F., Nahamuta Mashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Soki Y., Papellio H., Takemeto H., Walandamoto Y., Yano M.: Otherlio J. (FPP 1997) I. Her PMR 2004 SURVE (Attachases).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                       10.7%; Score 74; DB 2; Length 2449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%; Score 73; DB 2; Length 2383;
                                                                                          44; Indels
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247433 MW; E45P5PEE2AE76B59 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1997) to the EMBL/OchBank/DUBG databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251391 MW; 129975F4(PF64225C CRC64)
                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TremBirel, 02, Last sequence update)
01-MAR-2001 (TremBirel, 16, Last annotation update)
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                                                                                                                                                                                                                                          1605 EA . . - - - - VTFTLPADVSASFTLGQGGSALTDIN 1632
                                                                                                                                                                                                   96 NGAPISHATLVAFKYAWDVPPSFSI-- -- ISSDIN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENGAPISHATLVAFKYAWDVDPSFST----ISSDIN 126
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                                                                                            10; Mishatobos
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                                                                       Pred. No.
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                                                                          29.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D90837; BAA15800.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS: PR01369: INTIMIN. SMART; SM00089; PKI;; 1. SPQUENCE 2383 AA: 25139
                                                                                            Conservative
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Matches 28, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003535;
                                                                         Best Local Similarity
   2349 AA;
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     SECUENCE
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